GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 22:21:22 ; Search time 128 Seconds
(without alignments)
255.668 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgccactcccattctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 8

Total number of hits satisfying chosen parameters: 153720

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	827	4	US-10-121-857-56	Sequence 56, Appl
c	2	20	100.0	885	4	US-10-121-857-60	Sequence 60, Appl
c	3	20	100.0	2519	4	US-10-121-757B-7	Sequence 7, Appli
c	4	16	80.0	616	4	US-09-854-133-666	Sequence 666, App
c	5	15	75.0	508	4	US-09-621-976-1551	Sequence 1551, Ap
c	6	15	75.0	601	4	US-09-949-016-43149	Sequence 43149, A
c	7	15	75.0	601	4	US-09-949-016-43378	Sequence 43378, A
c	8	15	75.0	601	4	US-09-949-016-43607	Sequence 43607, A
c	9	15	75.0	601	4	US-09-949-016-117164	Sequence 117164,
c	10	15	75.0	1479	4	US-09-583-110-1385	Sequence 1385, Ap
c	11	15	75.0	1533	4	US-09-107-433-545	Sequence 545, App
	12	15	75.0	11303	3	US-08-961-527-115	Sequence 115, App
	13	15	75.0	80717	4	US-09-949-016-14968	Sequence 14968, A
c	14	15	75.0	89716	4	US-09-949-016-11900	Sequence 11900, A
	15	15	75.0	157866	4	US-09-949-016-12982	Sequence 12982, A
	16	15	75.0	157866	4	US-09-949-016-12983	Sequence 12983, A
	17	15	75.0	157866	4	US-09-949-016-12984	Sequence 12984, A
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	19	14	70.0	272	4	US-09-513-999C-33158	Sequence 33158, A
	20	14	70.0	601	4	US-09-949-016-82921	Sequence 82921, A
	21	14	70.0	601	4	US-09-949-016-82922	Sequence 82922, A
	22	14	70.0	601	4	US-09-949-016-132819	Sequence 132819,
	23	14	70.0	601	4	US-09-949-016-202121	Sequence 202121,
c	24	14	70.0	618	4	US-09-540-236-1580	Sequence 1580, Ap
c	25	14	70.0	751	4	US-09-687-698-14	Sequence 14, Appl
c	26	14	70.0	751	4	US-09-705-621-30	Sequence 30, Appl
	27	14	70.0	7417	4	US-09-573-080A-424	Sequence 424, App
c	28	14	70.0	7447	4	US-09-949-016-16540	Sequence 16540, A
	29	14	70.0	14551	4	US-09-949-016-12313	Sequence 12313, A
	30	14	70.0	14551	4	US-09-949-016-16465	Sequence 16465, A
	31	14	70.0	21535	4	US-09-949-016-12826	Sequence 12826, A
	32	14	70.0	21535	4	US-09-949-016-12827	Sequence 12827, A
	33	14	70.0	21535	4	US-09-949-016-12828	Sequence 12828, A
	34	14	70.0	21535	4	US-09-949-016-12829	Sequence 12829, A
	35	14	70.0	21536	4	US-09-949-016-13366	Sequence 13366, A
	36	14	70.0	21536	4	US-09-949-016-13367	Sequence 13367, A
	37	14	70.0	21536	4	US-09-949-016-13368	Sequence 13368, A
	38	14	70.0	21536	4	US-09-949-016-13369	Sequence 13369, A
c	39	14	70.0	34279	4	US-09-596-002-26	Sequence 26, Appl
	40	14	70.0	36542	4	US-09-949-016-12149	Sequence 12149, A
	41	14	70.0	36544	4	US-09-949-016-13434	Sequence 13434, A
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c	44	14	70.0	53336	4	US-09-949-016-12500	Sequence 12500, A
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	51	14	70.0	213456	4	US-09-820-007-3	Sequence 3, Appli
	52	14	70.0	246444	4	US-09-949-016-13113	Sequence 13113, A
	53	14	70.0	323820	4	US-09-949-016-14139	Sequence 14139, A
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c	55	14	70.0	1664976	4	US-09-692-570-1	Sequence 1, Appli
c	56	13	65.0	54	4	US-08-956-171E-2606	Sequence 2606, Ap
c	57	13	65.0	54	4	US-08-781-986A-2606	Sequence 2606, Ap
c	58	13	65.0	178	1	US-08-036-555B-138	Sequence 138, App
c	59	13	65.0	178	1	US-08-469-569-138	Sequence 138, App
c	60	13	65.0	178	1	US-08-249-322A-138	Sequence 138, App
c	61	13	65.0	178	1	US-08-469-526A-138	Sequence 138, App
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c	63	13	65.0	178	2	US-08-469-660-138	Sequence 138, App
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c	65	13	65.0	178	3	US-08-470-335-138	Sequence 138, App
c	66	13	65.0	178	3	US-08-735-021-138	Sequence 138, App
c	67	13	65.0	178	3	US-08-734-664A-138	Sequence 138, App
c	68	13	65.0	178	3	US-08-470-339-138	Sequence 138, App
c	69	13	65.0	178	3	US-08-467-602-138	Sequence 138, App
c	70	13	65.0	178	4	US-08-411-295F-12	Sequence 12, Appl
c	71	13	65.0	178	5	PCT-US94-05083C-134	Sequence 134, App
c	72	13	65.0	178	5	PCT-US95-06846A-138	Sequence 138, App
c	73	13	65.0	287	1	US-09-985-799-70	Sequence 70, Appl
c	74	13	65.0	287	1	US-09-977-371-70	Sequence 70, Appl
c	75	13	65.0	287	1	US-08-594-031-70	Sequence 70, Appl
	76	13	65.0	400	4	US-08-956-171E-1989	Sequence 1989, Ap
	77	13	65.0	400	4	US-08-781-986A-1989	Sequence 1989, Ap
	78	13	65.0	478	3	US-09-615-192A-131	Sequence 131, App
	79	13	65.0	478	4	US-09-169-789-131	Sequence 131, App
	80	13	65.0	483	4	US-09-621-976-13514	Sequence 13514, A
c	81	13	65.0	490	4	US-09-621-976-13659	Sequence 13659, A
	82	13	65.0	492	2	US-08-975-316-63	Sequence 63, Appl
	83	13	65.0	492	3	US-09-615-192A-63	Sequence 63, Appl
	84	13	65.0	492	4	US-09-169-789-63	Sequence 63, Appl
	85	13	65.0	572	4	US-09-270-767-219	Sequence 219, App
	86	13	65.0	572	4	US-09-270-767-15501	Sequence 15501, A
c	87	13	65.0	601	4	US-09-949-016-45144	Sequence 45144, A
c	88	13	65.0	601	4	US-09-949-016-45145	Sequence 45145, A
c	89	13	65.0	601	4	US-09-949-016-66326	Sequence 66326, A
	90	13	65.0	601	4	US-09-949-016-66940	Sequence 66940, A
	91	13	65.0	601	4	US-09-949-016-70882	Sequence 70882, A
	92	13	65.0	601	4	US-09-949-016-84085	Sequence 84085, A
	93	13	65.0	601	4	US-09-949-016-86882	Sequence 86882, A
	94	13	65.0	601	4	US-09-949-016-127701	Sequence 127701,
	95	13	65.0	601	4	US-09-949-016-127702	Sequence 127702,
	96	13	65.0	601	4	US-09-949-016-128038	Sequence 128038,
	97	13	65.0	601	4	US-09-949-016-128039	Sequence 128039,
	98	13	65.0	601	4	US-09-949-016-157982	Sequence 157982,
	99	13	65.0	601	4	US-09-949-016-157983	Sequence 157983,
	100	13	65.0	601	4	US-09-949-016-157984	Sequence 157984,

ALIGNMENTS

RESULT 1
US-10-121-857-56/c
; Sequence 56, Application US/10121857
; Patent No. 6822141
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.143
; CURRENT APPLICATION NUMBER: US/10/121,857
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 827
; TYPE: DNA
; ORGANISM: Human
US-10-121-857-56

Query Match 100.0%; Score 20; DB 4; Length 827;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 479 GCATTGCCACTCCCATTCTT 460

RESULT 2
US-10-121-857-60/c
; Sequence 60, Application US/10121857
; Patent No. 6822141
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.143
; CURRENT APPLICATION NUMBER: US/10/121,857
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 885
; TYPE: DNA
; ORGANISM: murine
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(885)
; OTHER INFORMATION: unsure at all n locations
US-10-121-857-60

Query Match 100.0%; Score 20; DB 4; Length 885;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 482 GCATTGCCACTCCCATTCTT 463

RESULT 3
US-10-121-757B-7/c
; Sequence 7, Application US/10121757B
; Patent No. 6835556
; GENERAL INFORMATION:
; APPLICANT: Attersand, Anneli
; TITLE OF INVENTION: Protein Cluster V
; FILE REFERENCE: 10806-164
; CURRENT APPLICATION NUMBER: US/10/121,757B
; CURRENT FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2519
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (714)..(1373)
; OTHER INFORMATION:
US-10-121-757B-7

Query Match 100.0%; Score 20; DB 4; Length 2519;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 904 GCATTGCCACTCCCATTCTT 885

RESULT 4
US-09-854-133-666/c
; Sequence 666, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 666
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-854-133-666

Query Match 80.0%; Score 16; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATTGCCACTCCCATTC 18
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Db 601 ATTGCCACTCCCATTC 586

RESULT 5
US-09-621-976-1551/c
; Sequence 1551, Application US/09621976
; Patent No. 6639063

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; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 1551
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 43..360
;   NAME/KEY: sig_peptide
;   LOCATION: 43..144
;   OTHER INFORMATION: Von Heijne matrix
;   OTHER INFORMATION: score 6.19999980926514
;   OTHER INFORMATION: seq LCLWTGECAPVLG/SP
US-09-621-976-1551

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
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Db        313 TGCCACTCCCATTCT 299


RESULT 6
US-09-949-016-43149/c
; Sequence 43149, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43149
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-43149

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  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db        578 TGCCACTCCCATTCT 564


RESULT 7
US-09-949-016-43378/c
; Sequence 43378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43378
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-43378

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  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
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Db        578 TGCCACTCCCATTCT 564


RESULT 8
US-09-949-016-43607/c
; Sequence 43607, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43607
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-43607

  Query Match             75.0%;  Score 15;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
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Db        578 TGCCACTCCCATTCT 564


RESULT 9
US-09-949-016-117164/c
; Sequence 117164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
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;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117164
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-117164

  Query Match             75.0%;  Score 15;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 ATTGCCACTCCCATT 17
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Db         95 ATTGCCACTCCCATT 81


RESULT 10
US-09-583-110-1385/c
; Sequence 1385, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;  APPLICANT:  Lynn Doucette-Stamm et al.
;  TITLE OF INVENTION:  Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE:  PATH00-07A
;  CURRENT APPLICATION NUMBER: US/09/583,110
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 09/107,433
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/085,131
;  PRIOR FILING DATE:  1998-05-12
;  PRIOR APPLICATION NUMBER:  US 60/051,553
;  PRIOR FILING DATE:  1997-07-02
;  NUMBER OF SEQ ID NOS:  5322
; SEQ ID NO 1385
;   LENGTH: 1479
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-1385

  Query Match             75.0%;  Score 15;  DB 4;  Length 1479;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TTGCCACTCCCATTC 18
              |||||||||||||||
Db       1092 TTGCCACTCCCATTC 1078


RESULT 11
US-09-107-433-545/c
; Sequence 545, Application US/09107433
; Patent No. 6800744
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: <Unknown>
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,433
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/ 085131
;             FILING DATE: May 12, 1998
;             APPLICATION NUMBER: 60/051553
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-011
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 545:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1533 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Streptococcus pneumoniae
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...1533
;        SEQUENCE DESCRIPTION: SEQ ID NO: 545:
US-09-107-433-545

  Query Match             75.0%;  Score 15;  DB 4;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TTGCCACTCCCATTC 18
              |||||||||||||||
Db       1146 TTGCCACTCCCATTC 1132


RESULT 12
US-08-961-527-115
; Sequence 115, Application US/08961527
; Patent No. 6420135
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Streptococcus pneumoniae Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  391
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,527
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  115:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11303 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-527-115

  Query Match             75.0%;  Score 15;  DB 3;  Length 11303;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TTGCCACTCCCATTC 18
              |||||||||||||||
Db       9199 TTGCCACTCCCATTC 9213


RESULT 13
US-09-949-016-14968
; Sequence 14968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14968
;   LENGTH: 80717
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(80717)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14968

  Query Match             75.0%;  Score 15;  DB 4;  Length 80717;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 ATTGCCACTCCCATT 17
              |||||||||||||||
Db      35880 ATTGCCACTCCCATT 35894


RESULT 14
US-09-949-016-11900/c
; Sequence 11900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11900
;   LENGTH: 89716
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(89716)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11900

  Query Match             75.0%;  Score 15;  DB 4;  Length 89716;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db      13066 TGCCACTCCCATTCT 13052


RESULT 15
US-09-949-016-12982
; Sequence 12982, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12982
;   LENGTH: 157866
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12982

  Query Match             75.0%;  Score 15;  DB 4;  Length 157866;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db      16979 TGCCACTCCCATTCT 16993


RESULT 16
US-09-949-016-12983
; Sequence 12983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
```

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12983
;   LENGTH: 157866
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12983

  Query Match             75.0%;  Score 15;  DB 4;  Length 157866;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db      16979 TGCCACTCCCATTCT 16993


RESULT 17
US-09-949-016-12984
; Sequence 12984, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12984
;   LENGTH: 157866
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12984

  Query Match             75.0%;  Score 15;  DB 4;  Length 157866;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db      16979 TGCCACTCCCATTCT 16993


RESULT 18
US-09-949-016-15779/c
; Sequence 15779, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15779
;   LENGTH: 265038
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(265038)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15779

  Query Match             75.0%;  Score 15;  DB 4;  Length 265038;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTCT 19
              |||||||||||||||
Db     195654 TGCCACTCCCATTCT 195640


RESULT 19
US-09-513-999C-33158
; Sequence 33158, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 33158
;   LENGTH: 272
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-33158

  Query Match             70.0%;  Score 14;  DB 4;  Length 272;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db        214 CCACTCCCATTCTT 227


RESULT 20
US-09-949-016-82921
; Sequence 82921, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82921
```

```
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-82921

  Query Match             70.0%;  Score 14;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTC 18
              ||||||||||||||
Db        414 TGCCACTCCCATTC 427


RESULT 21
US-09-949-016-82922
; Sequence 82922, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82922
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-82922

  Query Match             70.0%;  Score 14;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTC 18
              ||||||||||||||
Db        396 TGCCACTCCCATTC 409


RESULT 22
US-09-949-016-132819
; Sequence 132819, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132819
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-132819

  Query Match             70.0%;  Score 14;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCC 14
              ||||||||||||||
Db        336 GCATTGCCACTCCC 349


RESULT 23
US-09-949-016-202121
; Sequence 202121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202121
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-202121

  Query Match             70.0%;  Score 14;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCA 15
              ||||||||||||||
Db         45 CATTGCCACTCCCA 58


RESULT 24
US-09-540-236-1580/c
; Sequence 1580, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1580
;   LENGTH: 618
;   TYPE: DNA
;   ORGANISM: M.catarrhalis
US-09-540-236-1580

  Query Match             70.0%;  Score 14;  DB 4;  Length 618;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db        399 CCACTCCCATTCTT 386


RESULT 25
US-09-687-698-14/c
; Sequence 14, Application US/09687698
```

```
; Patent No. 6534067
; GENERAL INFORMATION:
;  APPLICANT:  Estes, Mary
;  TITLE OF INVENTION:   A NOVEL ADJUVANT
;  FILE REFERENCE:   P01883US1
;  CURRENT APPLICATION NUMBER: US/09/687,698
;  CURRENT FILING DATE:  2000-10-13
;  PRIOR APPLICATION NUMBER:   US 60/159,390
;  PRIOR FILING DATE:   1999-10-14
;  NUMBER OF SEQ ID NOS:   25
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 751
;   TYPE: DNA
;   ORGANISM: Bovine rotavirus strain B223
US-09-687-698-14

  Query Match             70.0%;  Score 14;  DB 4;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db        524 CCACTCCCATTCTT 511


RESULT 26
US-09-705-621-30/c
; Sequence 30, Application US/09705621
; Patent No. 6673355
; GENERAL INFORMATION:
;  APPLICANT:  ESTES, MARY
;  TITLE OF INVENTION:   ROTAVIRUS ENTEROTOXIN NSP4 AND METHODS OF USING SAME
;  FILE REFERENCE:   P01932US3
;  CURRENT APPLICATION NUMBER: US/09/705,621
;  CURRENT FILING DATE:  2000-11-03
;  NUMBER OF SEQ ID NOS:   39
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 751
;   TYPE: DNA
;   ORGANISM: Bovine Rotavirus Strain B223
US-09-705-621-30

  Query Match             70.0%;  Score 14;  DB 4;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db        524 CCACTCCCATTCTT 511


RESULT 27
US-09-573-080A-424
; Sequence 424, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
;  APPLICANT:  JOAN, KNOLL
;  APPLICANT:  ROGAN, PETER
;  TITLE OF INVENTION:   SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
;  FILE REFERENCE:   30307
;  CURRENT APPLICATION NUMBER: US/09/573,080A
;  CURRENT FILING DATE:  2000-05-16
;  NUMBER OF SEQ ID NOS:   479
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 424
;   LENGTH: 7417
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(7417)
;   OTHER INFORMATION: hervk14ci
;  PUBLICATION INFORMATION:
;  PUBLICATION INFORMATION:
;   AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
;   TITLE: Prototypic sequences for human repetitive DNA
;   JOURNAL: Journal of Molecular Evolution
;   VOLUME: 35
;   ISSUE: 4
;   PAGES: 286-291
;   DATE: 1992-10-__
;   DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
;   DATABASE ENTRY DATE: ____-__-__
;   DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-424

  Query Match             70.0%;  Score 14;  DB 4;  Length 7417;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TTGCCACTCCCATT 17
              ||||||||||||||
Db        712 TTGCCACTCCCATT 725


RESULT 28
US-09-949-016-16540/c
; Sequence 16540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16540
;   LENGTH: 7447
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16540

  Query Match             70.0%;  Score 14;  DB 4;  Length 7447;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTC 18
              ||||||||||||||
Db       5887 TGCCACTCCCATTC 5874


RESULT 29
US-09-949-016-12313
; Sequence 12313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
```

```
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12313
;    LENGTH: 14551
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12313

  Query Match             70.0%;  Score 14;  DB 4;  Length 14551;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GCCACTCCCATTCT 19
              ||||||||||||||
Db      10939 GCCACTCCCATTCT 10952


RESULT 30
US-09-949-016-16465
; Sequence 16465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16465
;    LENGTH: 14551
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-16465

  Query Match             70.0%;  Score 14;  DB 4;  Length 14551;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GCCACTCCCATTCT 19
              ||||||||||||||
Db      10939 GCCACTCCCATTCT 10952


RESULT 31
US-09-949-016-12826
; Sequence 12826, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12826
;    LENGTH: 21535
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12826

  Query Match             70.0%;  Score 14;  DB 4;  Length 21535;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 32
US-09-949-016-12827
; Sequence 12827, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12827
;    LENGTH: 21535
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12827

  Query Match             70.0%;  Score 14;  DB 4;  Length 21535;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 33
US-09-949-016-12828
; Sequence 12828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12828
;    LENGTH: 21535
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12828
```

```
  Query Match             70.0%;  Score 14;  DB 4;  Length 21535;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 34
US-09-949-016-12829
; Sequence 12829, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12829
;   LENGTH: 21535
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12829

  Query Match             70.0%;  Score 14;  DB 4;  Length 21535;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 35
US-09-949-016-13366
; Sequence 13366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13366
;   LENGTH: 21536
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13366

  Query Match             70.0%;  Score 14;  DB 4;  Length 21536;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 36
US-09-949-016-13367
; Sequence 13367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13367
;   LENGTH: 21536
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13367

  Query Match             70.0%;  Score 14;  DB 4;  Length 21536;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 37
US-09-949-016-13368
; Sequence 13368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13368
;   LENGTH: 21536
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13368

  Query Match             70.0%;  Score 14;  DB 4;  Length 21536;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 38
```

```
US-09-949-016-13369
; Sequence 13369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13369
;   LENGTH: 21536
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13369

  Query Match             70.0%;  Score 14;  DB 4;  Length 21536;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      13459 CCACTCCCATTCTT 13472


RESULT 39
US-09-596-002-26/c
; Sequence 26, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
;  APPLICANT:      Lagace, Robert, E.
;  APPLICANT:  Patterson, Chandra
;  APPLICANT:  Berg, Kim, L.
;  TITLE OF INVENTION:  NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
;  FILE REFERENCE:  PM-0008-4 US
;  CURRENT APPLICATION NUMBER: US/09/596,002
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER:  60/140,121
;  PRIOR FILING DATE:  1999-06-18
;  NUMBER OF SEQ ID NOS:  41
;  SOFTWARE:  PERL Program
; SEQ ID NO 26
;   LENGTH: 34279
;   TYPE: DNA
;   ORGANISM: M. catarrhalis
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte template ID No. 6632636 26
;  PUBLICATION INFORMATION:
US-09-596-002-26

  Query Match             70.0%;  Score 14;  DB 4;  Length 34279;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db       9394 CCACTCCCATTCTT 9381


RESULT 40
US-09-949-016-12149
; Sequence 12149, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12149
;   LENGTH: 36542
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12149

  Query Match             70.0%;  Score 14;  DB 4;  Length 36542;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      35042 CCACTCCCATTCTT 35055


RESULT 41
US-09-949-016-13434
; Sequence 13434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13434
;   LENGTH: 36544
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13434

  Query Match             70.0%;  Score 14;  DB 4;  Length 36544;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCACTCCCATTCTT 20
              ||||||||||||||
Db      35042 CCACTCCCATTCTT 35055


RESULT 42
US-09-949-016-12324/c
; Sequence 12324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
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;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12324
;    LENGTH: 47818
;    TYPE: DNA
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(47818)
;    OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12324

  Query Match             70.0%;  Score 14;  DB 4;  Length 47818;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTC 18
              ||||||||||||||
Db       6301 TGCCACTCCCATTC 6288


RESULT 43
US-09-949-016-15166/c
; Sequence 15166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15166
;    LENGTH: 48480
;    TYPE: DNA
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(48480)
;    OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15166

  Query Match             70.0%;  Score 14;  DB 4;  Length 48480;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TGCCACTCCCATTC 18
              ||||||||||||||
Db       6301 TGCCACTCCCATTC 6288


RESULT 44
US-09-949-016-12500/c
; Sequence 12500, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12500
;    LENGTH: 53336
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-12500

  Query Match             70.0%;  Score 14;  DB 4;  Length 53336;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GCCACTCCCATTCT 19
              ||||||||||||||
Db      21679 GCCACTCCCATTCT 21666


RESULT 45
US-09-949-016-16092/c
; Sequence 16092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16092
;    LENGTH: 53337
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-16092

  Query Match             70.0%;  Score 14;  DB 4;  Length 53337;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GCCACTCCCATTCT 19
              ||||||||||||||
Db      21679 GCCACTCCCATTCT 21666


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 10:09:26 ; Search time 427 Seconds
(without alignments)
277.271 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgccactcccattctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	469	10	ADD49704	Add49704 Human lun
c	2	20	100.0	827	3	AAZ60383	Aaz60383 A diacylg
c	3	20	100.0	885	3	AAZ60387	Aaz60387 A diacylg
	4	20	100.0	1030	12	ADO42678	Ado42678 Human NOV
	5	20	100.0	1077	12	ADO42677	Ado42677 Human NOV
c	6	20	100.0	1167	6	ABL53626	Abl53626 Breast pr
c	7	20	100.0	1167	6	AAD46542	Aad46542 Mouse dia
c	8	20	100.0	1167	12	ADO15616	Ado15616 Mouse DGA
c	9	20	100.0	1172	12	ADO42254	Ado42254 Human NOV
c	10	20	100.0	1189	12	ADO42252	Ado42252 Human NOV
c	11	20	100.0	1189	12	ADO42258	Ado42258 Human NOV
c	12	20	100.0	1191	12	ADO42248	Ado42248 Human NOV
c	13	20	100.0	1191	12	ADO42244	Ado42244 Human NOV
c	14	20	100.0	1198	12	ADO42256	Ado42256 Human NOV
c	15	20	100.0	1207	12	ADO42250	Ado42250 Human NOV
c	16	20	100.0	1230	12	ADO42246	Ado42246 Human NOV
c	17	20	100.0	1230	12	ADO42679	Ado42679 Human NOV
c	18	20	100.0	1231	6	AAD46541	Aad46541 Human dia
c	19	20	100.0	1231	12	ADO15614	Ado15614 Human DGA
c	20	20	100.0	1233	6	AAD46549	Aad46549 Human DGA
c	21	20	100:0	1233	12	ADO15631	Ado15631 Human acy
c	22	20	100.0	1303	2	AAZ33556	Aaz33556 Human bre
	23	20	100.0	1510	13	ADR26804	Adr26804 Breast ca
c	24	20	100.0	1543	6	ABL53628	Abl53628 Breast pr
c	25	20	100.0	1570	3	AAA37103	Aaa37103 Human PRO
c	26	20	100.0	1570	4	AAF54409	Aaf54409 Primer #8
c	27	20	100.0	1570	4	AAS46092	Aas46092 Human DNA
c	28	20	100.0	1570	8	ACA89542	Aca89542 cDNA enco
c	29	20	100.0	1570	8	ACA73552	Aca73552 Human sec
c	30	20	100.0	1570	8	ACA05867	Aca05867 Human sec
c	31	20	100.0	1570	8	ACA66701	Aca66701 cDNA enco
c	32	20	100.0	1570	8	ACF20276	Acf20276 Human sec
c	33	20	100.0	1570	8	ACF19662	Acf19662 Human sec
c	34	20	100.0	1570	8	ACD21950	Acd21950 Human sec
c	35	20	100.0	1570	8	ACF13115	Acf13115 Human sec
c	36	20	100.0	1570	8	ACD25218	Acd25218 Human sec
c	37	20	100.0	1570	8	ACF00267	Acf00267 Human sec
c	38	20	100.0	1570	8	ACA72324	Aca72324 Novel hum
c	39	20	100.0	1570	8	ACD04848	Acd04848 Novel hum
c	40	20	100.0	1570	8	ACD18309	Acd18309 Human sec
c	41	20	100.0	1570	8	ACD08316	Acd08316 Human sec
c	42	20	100.0	1570	8	ACA88750	Aca88750 Novel hum
c	43	20	100.0	1570	8	ACA70192	Aca70192 Human sec
c	44	20	100.0	1570	8	ACD12414	Acd12414 Novel hum
c	45	20	100.0	1570	8	ACC74329	Acc74329 Human sec
c	46	20	100.0	1570	8	ACD15957	Acd15957 Human sec
c	47	20	100.0	1570	8	ACD25525	Acd25525 Novel hum
c	48	20	100.0	1570	8	ACD18002	Acd18002 Human sec
c	49	20	100.0	1570	8	ACC88289	Acc88289 Human sec
c	50	20	100.0	1570	8	ACD21643	Acd21643 Human sec
c	51	20	100.0	1570	8	ACD18710	Acd18710 Human sec
c	52	20	100.0	1570	8	ABX98320	Abx98320 Human cDN
c	53	20	100.0	1570	8	ACD14071	Acd14071 Human PRO
c	54	20	100.0	1570	8	ACD09851	Acd09851 Human sec
c	55	20	100.0	1570	8	ACC88596	Acc88596 Human sec
c	56	20	100.0	1570	8	ACD21336	Acd21336 Human sec
c	57	20	100.0	1570	8	ABX75708	Abx75708 Human cDN
c	58	20	100.0	1570	8	ABX97911	Abx97911 Human PRO
c	59	20	100.0	1570	8	ACA97387	Aca97387 Novel hum
c	60	20	100.0	1570	8	ACA57850	Aca57850 Human PRO
c	61	20	100.0	1570	8	ACD14378	Acd14378 Human PRO
c	62	20	100.0	1570	8	ACC91161	Acc91161 Human sec
c	63	20	100.0	1570	8	ACC88903	Acc88903 Human sec
c	64	20	100.0	1570	8	ACD07100	Acd07100 Human PRO
c	65	20	100.0	1570	8	ACA67551	Aca67551 Human PRO
c	66	20	100.0	1570	8	ACC81606	Acc81606 Human sec
c	67	20	100.0	1570	8	ACC89210	Acc89210 Human sec
c	68	20	100.0	1570	8	ACC86566	Acc86566 Human sec
c	69	20	100.0	1570	8	ACC89824	Acc89824 Human sec
c	70	20	100.0	1570	8	ACC93003	Acc93003 Human sec
c	71	20	100.0	1570	8	ACA72631	Aca72631 Human PRO
c	72	20	100.0	1570	8	ACA89149	Aca89149 Human sec
c	73	20	100.0	1570	8	ACA69885	Aca69885 Human sec
c	74	20	100.0	1570	8	ACA97028	Aca97028 Novel hum
c	75	20	100.0	1570	8	ACA91024	Aca91024 Novel hum
c	76	20	100.0	1570	8	ACA70806	Aca70806 Human sec
c	77	20	100.0	1570	8	ACA95316	Aca95316 Novel hum
c	78	20	100.0	1570	8	ACC86259	Acc86259 Human sec
c	79	20	100.0	1570	8	ACC90131	Acc90131 Human sec
c	80	20	100.0	1570	8	ACD12739	Acd12739 Human sec
c	81	20	100.0	1570	8	ACF19969	Acf19969 Human sec
c	82	20	100.0	1570	8	ABX76913	Abx76913 Human PRO
c	83	20	100.0	1570	8	ACA73245	Aca73245 Novel hum
c	84	20	100.0	1570	8	ACA68788	Aca68788 Novel hum
c	85	20	100.0	1570	8	ACA74632	Aca74632 cDNA enco
c	86	20	100.0	1570	8	ACA70499	Aca70499 Human sec
c	87	20	100.0	1570	8	ACD14685	Acd14685 Human PRO
c	88	20	100.0	1570	8	ACA68357	Aca68357 Novel hum
c	89	20	100.0	1570	8	ABX98822	Abx98822 Novel hum
c	90	20	100.0	1570	8	ACC81299	Acc81299 Human sec
c	91	20	100.0	1570	8	ACA95623	Aca95623 Novel hum
c	92	20	100.0	1570	8	ACD04541	Acd04541 Novel hum
c	93	20	100.0	1570	8	ACC87982	Acc87982 Human sec

c 94	20	100.0	1570	8	ACF12644	Acf12644	Human sec
c 95	20	100.0	1570	8	ACA96359	Aca96359	Human PRO
c 96	20	100.0	1570	8	ACA65133	Aca65133	Human PRO
c 97	20	100.0	1570	8	ACA73859	Aca73859	Human sec
c 98	20	100.0	1570	8	ACA74271	Aca74271	Novel hum
c 99	20	100.0	1570	8	ACA96666	Aca96666	Human PRO
c 100	20	100.0	1570	8	ACD10772	Acd10772	cDNA enco

ALIGNMENTS

RESULT 1
ADD49704/c
ID ADD49704 standard; cDNA; 469 BP.
XX
AC ADD49704;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human lung cancer associated cDNA 61594676.
XX
KW Human; ss; lung cancer antigen; cytostatic; lung cancer; gene therapy;
KW vaccine; T-cell; tumour.
XX
OS Homo sapiens.
XX
PN US2003194764-A1.
XX
PD 16-OCT-2003.
XX
PF 04-APR-2002; 2002US-00116712.
XX
PR 05-APR-2001; 2001US-0282289P.
PR 05-OCT-2001; 2001US-0327511P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Switzer A;
XX
DR WPI; 2003-844452/78.
XX
PT New isolated polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cancer, particularly lung cancer.
XX
PS Claim 1; SEQ ID NO 436; 250pp; English.
XX
CC The invention relates to an isolated polynucleotide (a) comprising any of
CC the 666 fully defined nucleotide sequences appearing as ADD49269 -
CC ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at
CC least 20 contiguous residues of (a); sequences that hybridise to (a)
CC under highly stringent conditions; sequences having at least 75 or 90%
CC identity to (a); or degenerate variants of (a). Also included are an
CC isolated polypeptide ((b)(comprising: sequences encoded by the new
CC polynucleotide; any of the 4 amino acid sequences fully defined in the
CC specification; or sequences having at least 70 or 90% identity to the
CC sequence in (a) or (b)), an expression vector comprising the above
CC polynucleotide operably linked to an expression control sequence, a host
CC cell transformed or transfected with the above expression vector, an
CC isolated antibody, or its antigen-binding fragment, that specifically
CC binds to the above polypeptide, an oligonucleotide that hybridises to the
CC above-mentioned nucleotide sequences under highly stringent conditions, a
CC fusion protein comprising at least one polypeptide cited above, detecting
CC the presence of a cancer in a patient (comprising: obtaining a biological
CC sample from the patient; contacting the biological sample with a binding
CC agent that binds to the polypeptide, or with the oligonucleotide cited
CC above; detecting in the sample an amount of the polypeptide that binds to
CC the binding agent, or an amount of a polynucleotide that hybridises to
CC the oligonucleotide; and comparing the amount of polypeptide, or
CC polynucleotide that hybridises to the oligonucleotide, to a predetermined
CC cut-off value and then determining the presence of a cancer in the
CC patient), a method for stimulating and/or expanding T-cells specific for
CC a tumour protein (comprising contacting T-cells with the above
CC polypeptide, polynucleotide or antigen-presenting cells that express the
CC polynucleotide, under conditions and for a time sufficient to permit the
CC stimulation and/or expansion of T-cells), an isolated T-cell population
CC comprising T-cells prepared by the method, a composition comprising a
CC first component selected from physiological carriers and
CC immunostimulants, and a second component selected from the above
CC polypeptide, polynucleotide, antibody, fusion protein, T-cell population
CC and antigen-presenting cells that express the above polypeptide,
CC stimulating an immune response in a patient (comprising administering to
CC the patient the above composition) treating lung cancer in a patient
CC (comprising administering to the patient the above composition and a
CC diagnostic kit (comprising: at least one oligonucleotide cited above; or
CC at least one antibody cited above and a detection reagent, where the
CC detection reagent comprises a reporter group). The composition and
CC methods are useful in diagnosing, preventing and treating cancer,
CC particularly lung cancer. The present sequence is a lung cancer-
CC associated antigen cDNA of the invention.
XX
SQ Sequence 469 BP; 105 A; 123 C; 136 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 269 GCATTGCCACTCCCATTCTT 250

RESULT 2
AAZ60383/c
ID AAZ60383 standard; DNA; 827 BP.
XX
AC AAZ60383;
XX
DT 05-MAY-2000 (first entry)
XX
DE A diacylglycerol acyl transferase related expressed sequence tag.
XX
KW Diacylglycerol acyl transferase; DAGAT; triacylglycerol; diacylglycerol;
KW fatty acyl substrate; lipid composition; plant cell; fatty acid;
KW plant seed oil; chylomicra; small intestine;
KW very low density lipoprotein; liver; energy storage; adipose tissue;
KW lipid absorption; plasma triglyceride level; adipogenesis;
KW protein kinase C; cancer; diabetes; cardiopulmonary disease;
KW atherosclerosis; adipocytosis; leukaemia; fibroblastoma;
KW metabolic disorder; obesity; lipid metabolism; fat absorption;
KW expressed sequence tag; Mortierella ramanniana; ss.
XX
OS Homo sapiens.
XX
PN WO200001713-A2.
XX
PD 13-JAN-2000.
XX
PF 30-JUN-1999; 99WO-US015243.
XX
PR 02-JUL-1998; 98US-0091631P.
PR 23-APR-1999; 99US-0130829P.
XX
PA (CALJ) CALGENE LLC.
XX
PI Lardizabal KD, Hawkins D, Thompson GA;
XX
DR WPI; 2000-170997/15.
XX
PT New Mortierella ramanniana DNA encoding diacylglyceroltransferase for
PT producing transgenic plants or for treating the enzyme associated
PT diseases.
XX
PS Claim 9; Page 104; 114pp; English.
XX
CC The present sequence represents a contig of expressed sequence tags

CC (ESTs) which are related to the Mortierella ramanniana diacylglycerol
CC acyl transferase (DAGAT) sequence. The DAGAT enzyme is active in the
CC formation of triacylglycerol from diacylglycerol and fatty acyl
CC substrates. The DNA sequences encoding DAGAT can be used to modify the
CC triacylglycerol and lipid composition of plant cells. The DAGAT DNA
CC sequences may be in sense or antisense orientations to enhance or
CC suppress activity of endogenous DAGAT. DAGAT constructs are useful for
CC genetically altering plants to produce a particular fatty acid in the
CC plant seed oil. Antagonists and agonists of DAGAT activity are useful as
CC DAGAT is important in the formation of chylomicra in small intestine,
CC very low density lipoprotein in liver and for storage of energy as
CC triacylglycerol in adipose tissue. Thus, inhibiting DAGAT activity in
CC small intestine, liver and adipose tissue will reduce lipid absorption
CC and plasma triglyceride levels and will decrease adipogenesis. Agonists
CC and antagonists are particularly useful in treating diseases associated
CC with altered cellular diacylglycerol concentration or protein kinase C
CC activity, including cancer, diabetes, cardiopulmonary diseases,
CC atherosclerosis, adipocytosis, leukaemia, fibroblastoma, metabolic
CC disorders, obesity and diseases associated with abnormal lipid metabolism
CC and fat absorption
XX
SQ Sequence 827 BP; 174 A; 230 C; 227 G; 196 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 827;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 479 GCATTGCCACTCCCATTCTT 460

RESULT 3
AAZ60387/c
ID AAZ60387 standard; DNA; 885 BP.
XX
AC AAZ60387;
XX
DT 05-MAY-2000 (first entry)
XX
DE A diacylglycerol acyl transferase related expressed sequence tag.
XX
KW Diacylglycerol acyl transferase; DAGAT; triacylglycerol; diacylglycerol;
KW fatty acyl substrate; lipid composition; plant cell; fatty acid;
KW plant seed oil; chylomicra; small intestine;
KW very low density lipoprotein; liver; energy storage; adipose tissue;
KW lipid absorption; plasma triglyceride level; adipogenesis;
KW protein kinase C; cancer; diabetes; cardiopulmonary disease;
KW atherosclerosis; adipocytosis; leukaemia; fibroblastoma;
KW metabolic disorder; obesity; lipid metabolism; fat absorption;
KW expressed sequence tag; Mortierella ramanniana; ss.
XX
OS Mus sp.
XX
PN WO200001713-A2.
XX
PD 13-JAN-2000.
XX
PF 30-JUN-1999; 99WO-US015243.
XX
PR 02-JUL-1998; 98US-0091631P.
PR 23-APR-1999; 99US-0130829P.
XX
PA (CALJ) CALGENE LLC.
XX
PI Lardizabal KD, Hawkins D, Thompson GA;
XX
DR WPI; 2000-170997/15.
XX
PT New Mortierella ramanniana DNA encoding diacylglyceroltransferase for
PT producing transgenic plants or for treating the enzyme associated
PT diseases.
XX
PS Claim 9; Page 105; 114pp; English.
XX
CC The present sequence represents a contig of expressed sequence tags
CC (ESTs) which are related to the Mortierella ramanniana diacylglycerol
CC acyl transferase (DAGAT) sequence. The DAGAT enzyme is active in the
CC formation of triacylglycerol from diacylglycerol and fatty acyl
CC substrates. The DNA sequences encoding DAGAT can be used to modify the
CC triacylglycerol and lipid composition of plant cells. The DAGAT DNA
CC sequences may be in sense or antisense orientations to enhance or
CC suppress activity of endogenous DAGAT. DAGAT constructs are useful for
CC genetically altering plants to produce a particular fatty acid in the
CC plant seed oil. Antagonists and agonists of DAGAT activity are useful as
CC DAGAT is important in the formation of chylomicra in small intestine,
CC very low density lipoprotein in liver and for storage of energy as
CC triacylglycerol in adipose tissue. Thus, inhibiting DAGAT activity in
CC small intestine, liver and adipose tissue will reduce lipid absorption
CC and plasma triglyceride levels and will decrease adipogenesis. Agonists
CC and antagonists are particularly useful in treating diseases associated
CC with altered cellular diacylglycerol concentration or protein kinase C
CC activity, including cancer, diabetes, cardiopulmonary diseases,
CC atherosclerosis, adipocytosis, leukaemia, fibroblastoma, metabolic
CC disorders, obesity and diseases associated with abnormal lipid metabolism
CC and fat absorption
XX
SQ Sequence 885 BP; 190 A; 246 C; 240 G; 204 T; 0 U; 5 Other;

Query Match 100.0%; Score 20; DB 3; Length 885;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 482 GCATTGCCACTCCCATTCTT 463

RESULT 4
ADO42678
ID ADO42678 standard; cDNA; 1030 BP.
XX
AC ADO42678;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX-related polynucleotide #9.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.

PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
PR 14-DEC-2001; 2001US-0340608P.
PR 14-DEC-2001; 2001US-0341144P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 18-DEC-2001; 2001US-0341768P.
PR 20-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
PR 01-FEB-2002; 2002US-0353288P.
PR 26-FEB-2002; 2002US-0359599P.
PR 26-FEB-2002; 2002US-0359626P.
PR 26-FEB-2002; 2002US-0359671P.
PR 27-FEB-2002; 2002US-0359914P.
PR 27-FEB-2002; 2002US-0359956P.
PR 28-FEB-2002; 2002US-0360924P.
PR 28-FEB-2002; 2002US-0360964P.
PR 28-FEB-2002; 2002US-0361028P.
PR 28-FEB-2002; 2002US-0361256P.
PR 28-FEB-2002; 2002US-0361264P.
PR 05-MAR-2002; 2002US-0361770P.
PR 05-MAR-2002; 2002US-0362230P.
PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364238P.
PR 15-MAR-2002; 2002US-0364978P.
PR 15-MAR-2002; 2002US-0365025P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 16-MAY-2002; 2002US-0381004P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 02-JUL-2002; 2002US-0393332P.
PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
PR 20-AUG-2002; 2002US-0404676P.
PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
PR 23-AUG-2002; 2002US-0405687P.
PR 23-AUG-2002; 2002US-0405698P.
PR 26-AUG-2002; 2002US-0406353P.
XX
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Example E; SEQ ID NO 539; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX-related polynucleotide of the invention.
XX
SQ Sequence 1030 BP; 235 A; 292 C; 286 G; 217 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 274 GCATTGCCACTCCCATTCTT 293

RESULT 5
ADO42677
ID ADO42677 standard; cDNA; 1077 BP.
XX
AC ADO42677;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX-related polynucleotide #8.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;

KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
PR 14-DEC-2001; 2001US-0340608P.
PR 14-DEC-2001; 2001US-0341144P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 18-DEC-2001; 2001US-0341768P.
PR 20-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
PR 01-FEB-2002; 2002US-0353288P.
PR 26-FEB-2002; 2002US-0359599P.
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PR 26-FEB-2002; 2002US-0359671P.
PR 27-FEB-2002; 2002US-0359914P.
PR 27-FEB-2002; 2002US-0359956P.
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PR 05-MAR-2002; 2002US-0361770P.
PR 05-MAR-2002; 2002US-0362230P.
PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364238P.
PR 15-MAR-2002; 2002US-0364978P.
PR 15-MAR-2002; 2002US-0365025P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 16-MAY-2002; 2002US-0381004P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
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PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
PR 20-AUG-2002; 2002US-0404676P.
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PA (ANDE/) ANDERSON D W.
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PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
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PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
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PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Example E; SEQ ID NO 538; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX-related polynucleotide of the invention.

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XX
SQ   Sequence 1077 BP; 238 A; 295 C; 311 G; 233 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 12;  Length 1077;
  Best Local Similarity  100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        384 GCATTGCCACTCCCATTCTT 403


RESULT 6
ABL53626/c
ID   ABL53626 standard; cDNA; 1167 BP.
XX
AC   ABL53626;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.
XX
KW   BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;
KW   cytostatic; differential expression; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1167
FT                   /*tag=  a
FT                   /product= "BSTP-ECG1"
XX
PN   WO200208260-A2.
XX
PD   31-JAN-2002.
XX
PF   26-JUL-2001; 2001WO-US023439.
XX
PR   26-JUL-2000; 2000US-0220967P.
PR   06-DEC-2000; 2000US-0251669P.
XX
PA   (STRD ) UNIV STANFORD.
PA   (GENO-) APPLIED GENOMICS INC.
XX
PI   Botstein D,  Brown PO,  Perou C,  Ross D,  Seitz R;
XX
DR   WPI; 2002-315251/35.
DR   P-PSDB; ABB75677.
XX
PT   Novel substantially purified polypeptide encoded by breast protein-
PT   eukaryotic conserved gene 1, useful for diagnosing, treating or
PT   preventing breast cancer, and for classifying cancer.
XX
PS   Claim 2; Fig 1B; 127pp; English.
XX
CC   The present sequence is that of the coding region of BSTP-ECG1 (breast
CC   protein-eukaryotic conserved gene 1) cDNA, which encodes a 388-amino acid
CC   protein (see ABB75677). In order to identify genes that are
CC   differentially expressed in breast tumours, cDNA microarrays were
CC   produced, each representing the same set of approximately 8100 different
CC   human genes. Variations in patterns of gene expression were characterised
CC   in 62 breast tumour samples from 40 patients, 3 normal breast tissue
CC   samples and 19 samples from 17 human cell lines. IMAGE clone 161484 was
CC   identified based on the expression pattern of its mRNA among these 84
CC   samples. Overlapping clones (IMAGE clones 48805, 1276329, 1343900 and
CC   1560906) were identified in a database search, and a consensus sequence
CC   (see ABL53629) was produced, from which the present coding region is
CC   derived. BSTP-ECG1 is differentially expressed among breast tumours. The
CC   discovery of BSTP-ECG1 and its differential expression are useful for the
CC   diagnosis, treatment and prevention of cancer, especially breast cancer,
CC   and provides methods useful in tumour classification and prognosis. BSTP-
CC   ECG1 is probably a transmembrane protein, making it accessible to
CC   therapeutic agents such as antibodies and/or small molecules. The gene
CC   may also be a useful target for therapeutic intervention. The invention
CC   provides BSTP-ECG1 polypeptides and polynucleotides, expression vectors,
CC   host cells, antibodies, agonists and antagonists. It also provides
CC   methods for treating or preventing disorders of cell proliferation,
CC   particularly breast cancer, by administering a polypeptide,
CC   polynucleotide or antibody of the invention. Also provided are methods of
CC   classifying diseases, particularly breast cancer by detecting expression
CC   of BSTP-ECG1 or a polynucleotide encoding it, and of providing
CC   diagnostic, prognostic and/or predictive information for a patient based
CC   on the detection and/or measurement of BSTP-ECG1 or polynucleotide
CC   encoding BSTP-ECG1
XX
SQ   Sequence 1167 BP; 247 A; 338 C; 327 G; 255 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 6;  Length 1167;
  Best Local Similarity  100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 7
AAD46542/c
ID   AAD46542 standard; cDNA; 1167 BP.
XX
AC   AAD46542;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Mouse diacylglycerol acyltransferase (DGAT) 2alpha cDNA.
XX
KW   Mouse; monoacylglycerol acyltransferase; MGAT; hypertriglycaemia; DGAT;
KW   diacylglycerol acyltransferase; obesity; anorectic; hypoglycaemic;
KW   enzyme; gene; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1167
FT                   /*tag=  a
FT                   /product= "Mouse DGAT2alpha protein"
FT                   /transl_except= (pos:58. .60, aa:Leu)
FT                   /transl_except= (pos:61. .63, aa:Pro)
FT                   /transl_except= (pos:64. .66, aa:Ala)
FT                   /transl_except= (pos:67. .69, aa:Ala)
FT                   /transl_except= (pos:70. .72, aa:Lys)
FT                   /transl_except= (pos:643. .645, aa:Leu)
FT                   /transl_except= (pos:895. .903, aa:Val-Lys)
XX
PN   WO200268595-A2.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005474.
XX
PR   23-FEB-2001; 2001US-0271307P.
PR   26-FEB-2001; 2001US-00794715.
PR   14-JAN-2002; 2002US-00046924.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cases S,  Stone S,  Zhou P,  Farese RV,  Yen CE;
XX
DR   WPI; 2002-723199/78.
DR   P-PSDB; AAE29027.
XX
PT   New mammalian polynucleotide encoding a polypeptide that exhibits
PT   monoacylglycerol and/or diacylglycerol transferase activity, useful for
PT   treating a disease condition e.g. hypertriglycemia or obesity.
XX
PS   Claim 1; Fig 6B; 85pp; English.
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XX
CC   The invention relates to a mammalian polynucleotide present in other than
CC   its natural environment and encodes a polypeptide that exhibits
CC   monoacylglycerol (MGAT; E.C. 2.3.1.22) and/or diacylglycerol
CC   acyltransferase activity (DGAT; E.C. 2.3.1.20). The composition
CC   comprising the DGAT2alpha or MGAT1 polynucleotide or polypeptide is
CC   useful for treating a disease condition e.g. hypertriglycaemia or
CC   obesity. The present sequence is mouse DAGT2alpha cDNA
XX
SQ   Sequence 1167 BP; 258 A; 330 C; 320 G; 256 T; 0 U; 3 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 8
ADO15616/c
ID   ADO15616 standard; cDNA; 1167 BP.
XX
AC   ADO15616;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Mouse DGAT2alpha encoding cDNA SEQ ID NO:3.
XX
KW   monoacylglycerol acyltransferase; MGAT; EC 2.3.1.22;
KW   diacylglycerol transferase; DGAT; EC 2.3.1.20; enzyme; cardiovascular;
KW   anorectic; antilipaemic; antidiabetic; cytostatic; neuroprotective;
KW   diglyceride; triglyceride; acylglycerol metabolism;
KW   cardiovascular disease; hyperlipidaemia; obesity; diabetes; cancer;
KW   neurological disorder; immunological disorder; gene therapy; mouse;
KW   diacylglycerol O-acyltransferase 2 alpha; DGAT2alpha; gene; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1167
FT                   /*tag= a
FT                   /product= "DGAT2alpha"
FT                   /transl_except= (pos:58. .72,aa:LPAAK)
FT                   /transl_except= (pos:663. .665,aa:Leu)
FT                   /transl_except= (pos:898. .903,aa:Lys)
XX
PN   WO2004042014-A2.
XX
PD   21-MAY-2004.
XX
PF   29-OCT-2003; 2003WO-US034598.
XX
PR   31-OCT-2002; 2002US-00286581.
XX
PA   (GLAD-) GLADSTONE INST J DAVID.
XX
PI   Cases S,  Stone SJ,  Zhou P,  Farese RV,  Yen CE;
XX
DR   WPI; 2004-400668/37.
DR   P-PSDB; ADO15617.
XX
PT   New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for
PT   treating cardiovascular disease, hyperlipidemia, obesity, diabetes,
PT   cancer, neurological disorders and immunological disorders.
XX
PS   Example 1; SEQ ID NO 3; 98pp; English.
XX
CC   The present invention describes a mammalian monoacylglycerol
CC   acyltransferase (MGAT, EC 2.3.1.22) polypeptide (Ia) and a diacylglycerol
CC   transferase (DGAT, EC 2.3.1.20) polypeptide (Ib) present in other than
CC   its naturally occurring environment. Also described: (1) a mammalian
CC   polynucleotide (II) present in other than its natural environment
CC   encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an
CC   expression cassette (III) comprising a transcriptional initiation region
CC   functional in an expression host, (II) under the transcriptional
CC   regulation of the transcriptional initiation region, and transcriptional
CC   termination region functional in the expression host; (3) a cell (IV)
CC   comprising (III) as a part of an extrachromosomal element or integrated
CC   into the genome of a host cell as a result of introducing (III) into the
CC   host cell; (4) cellular progeny (V) of (IV); (5) preparing (Ia) and/or
CC   (Ib); (6) monoclonal antibody (VI) binding specifically to (Ia) or (Ib);
CC   (7) inhibiting (M1) the activity of (Ia) or (Ib); and (8) identifying an
CC   agent that inhibits an acyltransferase activity of MGAT2 polypeptide.
CC   (Ia) and (Ib) have cardiovascular, anorectic, antilipaemic, antidiabetic,
CC   cytostatic and neuroprotective activities. (Ia) can be used for producing
CC   in vitro models of diglyceride and/or triglyceride synthesis, and for
CC   producing triglyceride compositions which find use in foodstuffs,
CC   spreads, cooking materials, feedstocks and in industries for producing
CC   chemicals, lubricants and surfactants. (Ia), (Ib) and (VI) are useful for
CC   treating disease conditions associated with acylglycerol metabolism,
CC   particularly associated with diacylglycerol O-acyltransferase 2 alpha
CC   (DGAT2alpha), MGAT1 or MGAT2 activity. The disease conditions include
CC   cardiovascular disease, hyperlipidaemia, obesity, diabetes, cancer,
CC   neurological disorders and immunological disorders. (II) can be in gene
CC   therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2
CC   defects, as probes and primers in hybridisation applications (e.g., PCR),
CC   for identifying expression patterns in biological specimens, for
CC   preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,
CC   for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,
CC   to generate transgenic host. The present sequence encodes mouse
CC   DGAT2alpha, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 1167 BP; 258 A; 330 C; 320 G; 256 T; 0 U; 3 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 9
ADO42254/c
ID   ADO42254 standard; cDNA; 1172 BP.
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AC   ADO42254;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human NOVX polynucleotide #52.
XX
KW   Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW   Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW   scleroderma; hypertension; haemophilia;
KW   idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW   dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW   cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS   Homo sapiens.
XX
PN   US2004058338-A1.
XX
PD   25-MAR-2004.
XX
PF   02-DEC-2002; 2002US-00307817.
XX
PR   03-DEC-2001; 2001US-0336881P.
PR   05-DEC-2001; 2001US-0336820P.
PR   07-DEC-2001; 2001US-0338285P.
PR   07-DEC-2001; 2001US-0338318P.
PR   10-DEC-2001; 2001US-0338989P.
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PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
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PR 14-DEC-2001; 2001US-0340608P.
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PR 26-FEB-2002; 2002US-0359626P.
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PR 27-FEB-2002; 2002US-0359914P.
PR 27-FEB-2002; 2002US-0359956P.
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PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42255.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 103; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
SQ Sequence 1172 BP; 248 A; 343 C; 327 G; 254 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 703 GCATTGCCACTCCCATTCTT 684

RESULT 10
ADO42252/c
ID ADO42252 standard; cDNA; 1189 BP.
XX

AC ADO42252;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #51.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
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PR 18-DEC-2001; 2001US-0341768P.
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PR 05-MAR-2002; 2002US-0361770P.
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PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 02-JUL-2002; 2002US-0393332P.
PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
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PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
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PR 26-AUG-2002; 2002US-0406353P.
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PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
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PA (EDIN/) EDINGER S R.
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PA (ELLE/) ELLERMAN K.
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PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
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PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
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PA (KHRA/) KHRAMTSOV N V.
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PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
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PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42253.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 101; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX

```
CC   polypeptide. The sequences are useful for diagnosing, treating or
CC   preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC   diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC   disease, scleroderma, hypertension, haemophilia, idiopathic
CC   thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC   obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC   cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC   as hybridisation probes, in chromosome mapping, in tissue typing, in
CC   preventive medicine or in pharmacogenomics. This sequence represents a
CC   human NOVX polynucleotide of the invention.
XX
SQ   Sequence 1189 BP; 254 A; 351 C; 327 G; 257 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1189;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 11
ADO42258/c
ID   ADO42258 standard; cDNA; 1189 BP.
XX
AC   ADO42258;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human NOVX polynucleotide #54.
XX
KW   Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW   Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW   scleroderma; hypertension; haemophilia;
KW   idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW   dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW   cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS   Homo sapiens.
XX
PN   US2004058338-A1.
XX
PD   25-MAR-2004.
XX
PF   02-DEC-2002; 2002US-00307817.
XX
PR   03-DEC-2001; 2001US-0336881P.
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PR   07-DEC-2001; 2001US-0338285P.
PR   07-DEC-2001; 2001US-0338318P.
PR   10-DEC-2001; 2001US-0338989P.
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PR   11-DEC-2001; 2001US-0339516P.
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PR   12-DEC-2001; 2001US-0340981P.
PR   12-DEC-2001; 2001US-0341346P.
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PR   14-DEC-2001; 2001US-0341144P.
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PR   28-FEB-2002; 2002US-0361256P.
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PR   13-MAR-2002; 2002US-0364238P.
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PR   28-MAY-2002; 2002US-0383534P.
PR   28-MAY-2002; 2002US-0383744P.
PR   29-MAY-2002; 2002US-0383829P.
PR   29-MAY-2002; 2002US-0384024P.
PR   02-JUL-2002; 2002US-0393332P.
PR   06-AUG-2002; 2002US-0401315P.
PR   07-AUG-2002; 2002US-0401788P.
PR   20-AUG-2002; 2002US-0404676P.
PR   23-AUG-2002; 2002US-0405400P.
PR   23-AUG-2002; 2002US-0405684P.
PR   23-AUG-2002; 2002US-0405687P.
PR   23-AUG-2002; 2002US-0405698P.
PR   26-AUG-2002; 2002US-0406353P.
XX
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PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
```

PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
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PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42259.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 107; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
SQ Sequence 1189 BP; 254 A; 351 C; 327 G; 257 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 702 GCATTGCCACTCCCATTCTT 683

RESULT 12
ADO42248/c
ID ADO42248 standard; cDNA; 1191 BP.
XX
AC ADO42248;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #49.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
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PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
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PA (ROTH/) ROTHBERG B G.

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PA   (JIWW/) JI W.
PA   (KEKU/) KEKUDA R.
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PA   (ROTH/) ROTHENBERG M E.
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PA   (STON/) STONE D J.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZHON/) ZHONG M.
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PI   Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
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PI   Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI   Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI   Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR   WPI; 2004-268786/25.
DR   P-PSDB; AD042249.
XX
PT   New human NOVX polypeptides and nucleic acid molecules, useful for
PT   diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT   atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT   scleroderma.
XX
PS   Claim 20; SEQ ID NO 97; 610pp; English.
XX
CC   The invention relates to human NOVX polypeptides and the polynucleotides
CC   encoding them. The invention also relates to antibodies specific to the
CC   NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC   useful for manufacturing a medicament for treating a syndrome associated
CC   with a human disease, such as a pathology associated with the NOVX
CC   polypeptide. The sequences are useful for diagnosing, treating or
CC   preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC   diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC   disease, scleroderma, hypertension, haemophilia, idiopathic
CC   thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC   obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC   cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC   as hybridisation probes, in chromosome mapping, in tissue typing, in
CC   preventive medicine or in pharmacogenomics. This sequence represents a
CC   human NOVX polynucleotide of the invention.
XX
SQ   Sequence 1191 BP; 252 A; 345 C; 334 G; 260 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1191;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        722 GCATTGCCACTCCCATTCTT 703
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RESULT 13
AD042244/c
ID   AD042244 standard; cDNA; 1191 BP.
XX
AC   AD042244;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human NOVX polynucleotide #47.
XX
KW   Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW   Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW   scleroderma; hypertension; haemophilia;
KW   idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW   dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW   cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS   Homo sapiens.
XX
PN   US2004058338-A1.
XX
PD   25-MAR-2004.
XX
PF   02-DEC-2002; 2002US-00307817.
XX
PR   03-DEC-2001; 2001US-0336881P.
PR   05-DEC-2001; 2001US-0336820P.
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PR   31-DEC-2001; 2001US-0344903P.
PR   01-FEB-2002; 2002US-0353286P.
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PR   26-FEB-2002; 2002US-0359671P.
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PR   27-FEB-2002; 2002US-0359956P.
PR   28-FEB-2002; 2002US-0360924P.
PR   28-FEB-2002; 2002US-0360964P.
PR   28-FEB-2002; 2002US-0361028P.
PR   28-FEB-2002; 2002US-0361256P.
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PR   05-MAR-2002; 2002US-0361770P.
PR   05-MAR-2002; 2002US-0362230P.
PR   13-MAR-2002; 2002US-0364181P.
PR   13-MAR-2002; 2002US-0364238P.
PR   15-MAR-2002; 2002US-0364978P.
PR   15-MAR-2002; 2002US-0365025P.
PR   17-APR-2002; 2002US-0373288P.
PR   15-MAY-2002; 2002US-0380981P.
PR   16-MAY-2002; 2002US-0381004P.
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PR   28-MAY-2002; 2002US-0383744P.
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PR 29-MAY-2002; 2002US-0384024P.
PR 02-JUL-2002; 2002US-0393332P.
PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
PR 20-AUG-2002; 2002US-0404676P.
PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
PR 23-AUG-2002; 2002US-0405687P.
PR 23-AUG-2002; 2002US-0405698P.
PR 26-AUG-2002; 2002US-0406353P.
XX
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42245.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 93; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
SQ Sequence 1191 BP; 252 A; 345 C; 334 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 722 GCATTGCCACTCCCATTCTT 703

RESULT 14
ADO42256/c
ID ADO42256 standard; cDNA; 1198 BP.
XX
AC ADO42256;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #53.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
PR 14-DEC-2001; 2001US-0340608P.
PR 14-DEC-2001; 2001US-0341144P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 18-DEC-2001; 2001US-0341768P.
PR 20-DEC-2001; 2001US-0342592P.

PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
PR 01-FEB-2002; 2002US-0353288P.
PR 26-FEB-2002; 2002US-0359599P.
PR 26-FEB-2002; 2002US-0359626P.
PR 26-FEB-2002; 2002US-0359671P.
PR 27-FEB-2002; 2002US-0359914P.
PR 27-FEB-2002; 2002US-0359956P.
PR 28-FEB-2002; 2002US-0360924P.
PR 28-FEB-2002; 2002US-0360964P.
PR 28-FEB-2002; 2002US-0361028P.
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PR 28-FEB-2002; 2002US-0361264P.
PR 05-MAR-2002; 2002US-0361770P.
PR 05-MAR-2002; 2002US-0362230P.
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PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
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PR 20-AUG-2002; 2002US-0404676P.
PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
PR 23-AUG-2002; 2002US-0405687P.
PR 23-AUG-2002; 2002US-0405698P.
PR 26-AUG-2002; 2002US-0406353P.
XX
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PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
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PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
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PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42257.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 105; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
SQ Sequence 1198 BP; 251 A; 351 C; 332 G; 264 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1198;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 711 GCATTGCCACTCCCATTCTT 692

RESULT 15
ADO42250/c
ID ADO42250 standard; cDNA; 1207 BP.
XX
AC ADO42250;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #50.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.

XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
PR 14-DEC-2001; 2001US-0340608P.
PR 14-DEC-2001; 2001US-0341144P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 18-DEC-2001; 2001US-0341768P.
PR 20-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
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PR 28-FEB-2002; 2002US-0361028P.
PR 28-FEB-2002; 2002US-0361256P.
PR 28-FEB-2002; 2002US-0361264P.
PR 05-MAR-2002; 2002US-0361770P.
PR 05-MAR-2002; 2002US-0362230P.
PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364238P.
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PR 15-MAR-2002; 2002US-0365025P.
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PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
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PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
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PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
PR 23-AUG-2002; 2002US-0405687P.
PR 23-AUG-2002; 2002US-0405698P.
PR 26-AUG-2002; 2002US-0406353P.
XX
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42251.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT scleroderma.
XX
PS Claim 20; SEQ ID NO 99; 610pp; English.
XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The invention also relates to antibodies specific to the
CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC useful for manufacturing a medicament for treating a syndrome associated
CC with a human disease, such as a pathology associated with the NOVX
CC polypeptide. The sequences are useful for diagnosing, treating or
CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC disease, scleroderma, hypertension, haemophilia, idiopathic
CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC as hybridisation probes, in chromosome mapping, in tissue typing, in
CC preventive medicine or in pharmacogenomics. This sequence represents a
CC human NOVX polynucleotide of the invention.
XX
SQ Sequence 1207 BP; 258 A; 359 C; 332 G; 258 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1207;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        710 GCATTGCCACTCCCATTCTT 691
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RESULT 16
ADO42246/c
ID ADO42246 standard; cDNA; 1230 BP.
XX
AC ADO42246;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human NOVX polynucleotide #48.
XX
KW Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW scleroderma; hypertension; haemophilia;
KW idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS Homo sapiens.
XX
PN US2004058338-A1.
XX
PD 25-MAR-2004.
XX
PF 02-DEC-2002; 2002US-00307817.
XX
PR 03-DEC-2001; 2001US-0336881P.
PR 05-DEC-2001; 2001US-0336820P.
PR 07-DEC-2001; 2001US-0338285P.
PR 07-DEC-2001; 2001US-0338318P.
PR 10-DEC-2001; 2001US-0338989P.
PR 10-DEC-2001; 2001US-0339022P.
PR 11-DEC-2001; 2001US-0339314P.
PR 11-DEC-2001; 2001US-0339516P.
PR 11-DEC-2001; 2001US-0339517P.
PR 11-DEC-2001; 2001US-0339611P.
PR 12-DEC-2001; 2001US-0340981P.
PR 12-DEC-2001; 2001US-0341346P.
PR 14-DEC-2001; 2001US-0340390P.
PR 14-DEC-2001; 2001US-0340440P.
PR 14-DEC-2001; 2001US-0340565P.
PR 14-DEC-2001; 2001US-0340608P.
PR 14-DEC-2001; 2001US-0341144P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 18-DEC-2001; 2001US-0341768P.
PR 20-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344903P.
PR 01-FEB-2002; 2002US-0353286P.
PR 01-FEB-2002; 2002US-0353288P.
PR 26-FEB-2002; 2002US-0359599P.
PR 26-FEB-2002; 2002US-0359626P.
PR 26-FEB-2002; 2002US-0359671P.
PR 27-FEB-2002; 2002US-0359914P.
PR 27-FEB-2002; 2002US-0359956P.
PR 28-FEB-2002; 2002US-0360924P.
PR 28-FEB-2002; 2002US-0360964P.
PR 28-FEB-2002; 2002US-0361028P.
PR 28-FEB-2002; 2002US-0361256P.
PR 28-FEB-2002; 2002US-0361264P.
PR 05-MAR-2002; 2002US-0361770P.
PR 05-MAR-2002; 2002US-0362230P.
PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364238P.
PR 15-MAR-2002; 2002US-0364978P.
PR 15-MAR-2002; 2002US-0365025P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 16-MAY-2002; 2002US-0381004P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 02-JUL-2002; 2002US-0393332P.
PR 06-AUG-2002; 2002US-0401315P.
PR 07-AUG-2002; 2002US-0401788P.
PR 20-AUG-2002; 2002US-0404676P.
PR 23-AUG-2002; 2002US-0405400P.
PR 23-AUG-2002; 2002US-0405684P.
PR 23-AUG-2002; 2002US-0405687P.
PR 23-AUG-2002; 2002US-0405698P.
PR 26-AUG-2002; 2002US-0406353P.
XX
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
XX
PI Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khramtsov NV;
PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX
DR WPI; 2004-268786/25.
DR P-PSDB; ADO42247.
XX
PT New human NOVX polypeptides and nucleic acid molecules, useful for
PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,

```
PT   atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT   scleroderma.
XX
PS   Claim 20; SEQ ID NO 95; 610pp; English.
XX
CC   The invention relates to human NOVX polypeptides and the polynucleotides
CC   encoding them. The invention also relates to antibodies specific to the
CC   NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC   useful for manufacturing a medicament for treating a syndrome associated
CC   with a human disease, such as a pathology associated with the NOVX
CC   polypeptide. The sequences are useful for diagnosing, treating or
CC   preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC   diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC   disease, scleroderma, hypertension, haemophilia, idiopathic
CC   thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC   obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC   cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC   as hybridisation probes, in chromosome mapping, in tissue typing, in
CC   preventive medicine or in pharmacogenomics. This sequence represents a
CC   human NOVX polynucleotide of the invention.
XX
SQ   Sequence 1230 BP; 259 A; 359 C; 341 G; 271 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 17
ADO42679/c
ID   ADO42679 standard; cDNA; 1230 BP.
XX
AC   ADO42679;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human NOVX-related polynucleotide #10.
XX
KW   Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
KW   Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
KW   scleroderma; hypertension; haemophilia;
KW   idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
KW   dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
KW   cancer-associated cachexia; multiple sclerosis; fertility.
XX
OS   Homo sapiens.
XX
PN   US2004058338-A1.
XX
PD   25-MAR-2004.
XX
PF   02-DEC-2002; 2002US-00307817.
XX
PR   03-DEC-2001; 2001US-0336881P.
PR   05-DEC-2001; 2001US-0336820P.
PR   07-DEC-2001; 2001US-0338285P.
PR   07-DEC-2001; 2001US-0338318P.
PR   10-DEC-2001; 2001US-0338989P.
PR   10-DEC-2001; 2001US-0339022P.
PR   11-DEC-2001; 2001US-0339314P.
PR   11-DEC-2001; 2001US-0339516P.
PR   11-DEC-2001; 2001US-0339517P.
PR   11-DEC-2001; 2001US-0339611P.
PR   12-DEC-2001; 2001US-0340981P.
PR   12-DEC-2001; 2001US-0341346P.
PR   14-DEC-2001; 2001US-0340390P.
PR   14-DEC-2001; 2001US-0340440P.
PR   14-DEC-2001; 2001US-0340565P.
PR   14-DEC-2001; 2001US-0340608P.
PR   14-DEC-2001; 2001US-0341144P.
PR   17-DEC-2001; 2001US-0341477P.
PR   17-DEC-2001; 2001US-0341540P.
PR   18-DEC-2001; 2001US-0341768P.
PR   20-DEC-2001; 2001US-0342592P.
PR   31-DEC-2001; 2001US-0344903P.
PR   01-FEB-2002; 2002US-0353286P.
PR   01-FEB-2002; 2002US-0353288P.
PR   26-FEB-2002; 2002US-0359599P.
PR   26-FEB-2002; 2002US-0359626P.
PR   26-FEB-2002; 2002US-0359671P.
PR   27-FEB-2002; 2002US-0359914P.
PR   27-FEB-2002; 2002US-0359956P.
PR   28-FEB-2002; 2002US-0360924P.
PR   28-FEB-2002; 2002US-0360964P.
PR   28-FEB-2002; 2002US-0361028P.
PR   28-FEB-2002; 2002US-0361256P.
PR   28-FEB-2002; 2002US-0361264P.
PR   05-MAR-2002; 2002US-0361770P.
PR   05-MAR-2002; 2002US-0362230P.
PR   13-MAR-2002; 2002US-0364181P.
PR   13-MAR-2002; 2002US-0364238P.
PR   15-MAR-2002; 2002US-0364978P.
PR   15-MAR-2002; 2002US-0365025P.
PR   17-APR-2002; 2002US-0373288P.
PR   15-MAY-2002; 2002US-0380981P.
PR   16-MAY-2002; 2002US-0381004P.
PR   17-MAY-2002; 2002US-0381495P.
PR   28-MAY-2002; 2002US-0383534P.
PR   28-MAY-2002; 2002US-0383744P.
PR   29-MAY-2002; 2002US-0383829P.
PR   29-MAY-2002; 2002US-0384024P.
PR   02-JUL-2002; 2002US-0393332P.
PR   06-AUG-2002; 2002US-0401315P.
PR   07-AUG-2002; 2002US-0401788P.
PR   20-AUG-2002; 2002US-0404676P.
PR   23-AUG-2002; 2002US-0405400P.
PR   23-AUG-2002; 2002US-0405684P.
PR   23-AUG-2002; 2002US-0405687P.
PR   23-AUG-2002; 2002US-0405698P.
PR   26-AUG-2002; 2002US-0406353P.
XX
PA   (AGEE/) AGEE M L.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BERG/) BERGHS C.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CATT/) CATTERTON E.
PA   (DIPI/) DIPIPPO V A.
PA   (EDIN/) EDINGER S R.
PA   (EISE/) EISEN A.
PA   (ELLE/) ELLERMAN K.
PA   (GANG/) GANGOLLI E A.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (ROTH/) ROTHBERG B G.
PA   (GUOX/) GUO X S.
PA   (HERR/) HERRMANN J L.
PA   (HALV/) HALVORSEN Y.
PA   (JIWW/) JI W.
PA   (KEKU/) KEKUDA R.
PA   (KHRA/) KHRAMTSOV N V.
PA   (LARO/) LAROCHELLE W J.
PA   (LEPL/) LEPLEY D M.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MILL/) MILLER C E.
PA   (ORTT/) ORT T.
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PA   (PATT/) PATTURAJAN M.
PA   (PENA/) PENA C E A.
PA   (PEYM/) PEYMAN J A.
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PA   (RIEG/) RIEGER D K.
PA   (ROTH/) ROTHENBERG M E.
PA   (SHEN/) SHENOY S G.
PA   (SMIT/) SMITHSON G.
PA   (SPAD/) SPADERNA S K.
PA   (SPYT/) SPYTEK K A.
PA   (STON/) STONE D J.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZHON/) ZHONG M.
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PI   Agee ML,  Alsobrook JP,  Anderson DW,  Berghs C,  Boldog FL;
PI   Burgess CE,  Catterton E,  Dipippo VA,  Edinger SR,  Eisen A;
PI   Ellerman K,  Gangolli EA,  Gerlach V,  Gorman L,  Rothberg BG,  Guo XS;
PI   Herrmann JL,  Halvorsen Y,  Ji W,  Kekuda R,  Khramtsov NV;
PI   Larochelle WJ,  Lepley DM,  Li L,  Macdougall JR,  Miller CE,  Ort T;
PI   Padigaru M,  Patturajan M,  Pena CEA,  Peyman JA,  Rieger DK;
PI   Rothenberg ME,  Shenoy SG,  Smithson G,  Spaderna SK,  Spytek KA;
PI   Stone DJ,  Taupier RJ,  Vernet CAM,  Voss EZ,  Zhong M;
XX
DR   WPI; 2004-268786/25.
DR   P-PSDB; ADO42680.
XX
PT   New human NOVX polypeptides and nucleic acid molecules, useful for
PT   diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PT   atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PT   scleroderma.
XX
PS   Example E; SEQ ID NO 540; 610pp; English.
XX
CC   The invention relates to human NOVX polypeptides and the polynucleotides
CC   encoding them. The invention also relates to antibodies specific to the
CC   NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
CC   useful for manufacturing a medicament for treating a syndrome associated
CC   with a human disease, such as a pathology associated with the NOVX
CC   polypeptide. The sequences are useful for diagnosing, treating or
CC   preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
CC   diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
CC   disease, scleroderma, hypertension, haemophilia, idiopathic
CC   thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
CC   obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
CC   cachexia, multiple sclerosis or fertility. The nucleic acids may be used
CC   as hybridisation probes, in chromosome mapping, in tissue typing, in
CC   preventive medicine or in pharmacogenomics. This sequence represents a
CC   human NOVX-related polynucleotide of the invention.
XX
SQ   Sequence 1230 BP; 259 A; 359 C; 341 G; 271 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 18
AAD46541/c
ID   AAD46541 standard; cDNA; 1231 BP.
XX
AC   AAD46541;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human diacylglycerol acyltransferase (DGAT) 2alpha cDNA.
XX
KW   Human; monoacylglycerol acyltransferase; MGAT; hypertriglycaemia; DGAT;
KW   diacylglycerol acyltransferase; obesity; anorectic; hypoglycaemic;
KW   enzyme; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             7. .1171
FT                   /*tag=  a
FT                   /product= "Human DGAT2alpha protein"
FT                   /transl_except= (pos:98. .100, aa:Ala-Leu)
XX
PN   WO200268595-A2.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005474.
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PR   23-FEB-2001; 2001US-0271307P.
PR   26-FEB-2001; 2001US-00794715.
PR   14-JAN-2002; 2002US-00046924.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cases S,  Stone S,  Zhou P,  Farese RV,  Yen CE;
XX
DR   WPI; 2002-723199/78.
DR   P-PSDB; AAE29026.
XX
PT   New mammalian polynucleotide encoding a polypeptide that exhibits
PT   monoacylglycerol and/or diacylglycerol transferase activity, useful for
PT   treating a disease condition e.g. hypertriglycemia or obesity.
XX
PS   Claim 1; Fig 7B; 85pp; English.
XX
CC   The invention relates to a mammalian polynucleotide present in other than
CC   its natural environment and encodes a polypeptide that exhibits
CC   monoacylglycerol (MGAT; E.C. 2.3.1.22) and/or diacylglycerol
CC   acyltransferase activity (DGAT; E.C. 2.3.1.20). The composition
CC   comprising the DGAT2alpha or MGAT1 polynucleotide or polypeptide is
CC   useful for treating a disease condition e.g. hypertriglycaemia or
CC   obesity. The present sequence is human DAGT2alpha cDNA
XX
SQ   Sequence 1231 BP; 260 A; 359 C; 341 G; 271 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 19
ADO15614/c
ID   ADO15614 standard; cDNA; 1231 BP.
XX
AC   ADO15614;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human DGAT2alpha encoding cDNA SEQ ID NO:1.
XX
KW   monoacylglycerol acyltransferase; MGAT; EC 2.3.1.22;
KW   diacylglycerol transferase; DGAT; EC 2.3.1.20; enzyme; cardiovascular;
KW   anorectic; antilipaemic; antidiabetic; cytostatic; neuroprotective;
KW   diglyceride; triglyceride; acylglycerol metabolism;
KW   cardiovascular disease; hyperlipidaemia; obesity; diabetes; cancer;
KW   neurological disorder; immunological disorder; gene therapy; human;
KW   diacylglycerol O-acyltransferase 2 alpha; DGAT2alpha; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .1171
FT                   /*tag=  a
FT                   /product= "DGAT2alpha"
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FT                   /transl_except= (pos:98. .100,aa:AlaLeu)
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PN   WO2004042014-A2.
XX
PD   21-MAY-2004.
XX
PF   29-OCT-2003; 2003WO-US034598.
XX
PR   31-OCT-2002; 2002US-00286581.
XX
PA   (GLAD-) GLADSTONE INST J DAVID.
XX
PI   Cases S,  Stone SJ,  Zhou P,  Farese RV,  Yen CE;
XX
DR   WPI; 2004-400668/37.
DR   P-PSDB; ADO15615.
XX
PT   New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for
PT   treating cardiovascular disease, hyperlipidemia, obesity, diabetes,
PT   cancer, neurological disorders and immunological disorders.
XX
PS   Example 1; SEQ ID NO 1; 98pp; English.
XX
CC   The present invention describes a mammalian monoacylglycerol
CC   acyltransferase (MGAT, EC 2.3.1.22) polypeptide (Ia) and a diacylglycerol
CC   transferase (DGAT, EC 2.3.1.20) polypeptide (Ib) present in other than
CC   its naturally occurring environment. Also described: (1) a mammalian
CC   polynucleotide (II) present in other than its natural environment
CC   encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an
CC   expression cassette (III) comprising a transcriptional initiation region
CC   functional in an expression host, (II) under the transcriptional
CC   regulation of the transcriptional initiation region, and transcriptional
CC   termination region functional in the expression host; (3) a cell (IV)
CC   comprising (III) as a part of an extrachromosomal element or integrated
CC   into the genome of a host cell as a result of introducing (III) into the
CC   host cell; (4) cellular progeny (V) of (IV); (5) preparing (Ia) and/or
CC   (Ib); (6) monoclonal antibody (VI) binding specifically to (Ia) or (Ib);
CC   (7) inhibiting (M1) the activity of (Ia) or (Ib); and (8) identifying an
CC   agent that inhibits an acyltransferase activity of MGAT2 polypeptide.
CC   (Ia) and (Ib) have cardiovascular, anorectic, antilipaemic, antidiabetic,
CC   cytostatic and neuroprotective activities. (Ia) can be used for producing
CC   in vitro models of diglyceride and/or triglyceride synthesis, and for
CC   producing triglyceride compositions which find use in foodstuffs,
CC   spreads, cooking materials, feedstocks and in industries for producing
CC   chemicals, lubricants and surfactants. (Ia), (Ib) and (VI) are useful for
CC   treating disease conditions associated with acylglycerol metabolism,
CC   particularly associated with diacylglycerol O-acyltransferase 2 alpha
CC   (DGAT2alpha), MGAT1 or MGAT2 activity. The disease conditions include
CC   cardiovascular disease, hyperlipidaemia, obesity, diabetes, cancer,
CC   neurological disorders and immunological disorders. (II) can be in gene
CC   therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2
CC   defects, as probes and primers in hybridisation applications (e.g., PCR),
CC   for identifying expression patterns in biological specimens, for
CC   preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,
CC   for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,
CC   to generate transgenic host. The present sequence encodes human
CC   DGAT2alpha, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 1231 BP; 260 A; 359 C; 341 G; 271 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 20
AAD46549/c
ID   AAD46549 standard; DNA; 1233 BP.
XX
AC   AAD46549;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human DGAT/MGAT-related DNA.
XX
KW   Human; monoacylglycerol acyltransferase; MGAT; hypertriglycaemia; DGAT;
KW   diacylglycerol acyltransferase; obesity; anorectic; hypoglycaemic;
KW   enzyme; ds.
XX
OS   Homo sapiens.
XX
PN   WO200268595-A2.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005474.
XX
PR   23-FEB-2001; 2001US-0271307P.
PR   26-FEB-2001; 2001US-00794715.
PR   14-JAN-2002; 2002US-00046924.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cases S,  Stone S,  Zhou P,  Farese RV,  Yen CE;
XX
DR   WPI; 2002-723199/78.
XX
PT   New mammalian polynucleotide encoding a polypeptide that exhibits
PT   monoacylglycerol and/or diacylglycerol transferase activity, useful for
PT   treating a disease condition e.g. hypertriglycemia or obesity.
XX
PS   Claim 1; Page 82; 85pp; English.
XX
CC   The invention relates to a mammalian polynucleotide present in other than
CC   its natural environment and encodes a polypeptide that exhibits.
CC   monoacylglycerol (MGAT; E.C. 2.3.1.22) and/or diacylglycerol
CC   acyltransferase activity (DGAT; E.C. 2.3.1.20). The composition
CC   comprising the DGAT2alpha or MGAT1 polynucleotide or polypeptide is
CC   useful for treating a disease condition e.g. hypertriglycaemia or
CC   obesity. The present sequence is human DGAT/MGAT-related DNA
XX
SQ   Sequence 1233 BP; 259 A; 360 C; 342 G; 272 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 1233;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        705 GCATTGCCACTCCCATTCTT 686


RESULT 21
ADO15631/c
ID   ADO15631 standard; DNA; 1233 BP.
XX
AC   ADO15631;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human acylglycerol acyltransferase related nucleotide sequence SEQ ID:18.
XX
KW   monoacylglycerol acyltransferase; MGAT; EC 2.3.1.22;
KW   diacylglycerol transferase; DGAT; EC 2.3.1.20; enzyme; cardiovascular;
KW   anorectic; antilipaemic; antidiabetic; cytostatic; neuroprotective;
KW   diglyceride; triglyceride; acylglycerol metabolism;
KW   cardiovascular disease; hyperlipidaemia; obesity; diabetes; cancer;
KW   neurological disorder; immunological disorder; gene therapy; human; gene;
KW   ds.
XX
OS   Homo sapiens.
```

XX
PN WO2004042014-A2.
XX
PD 21-MAY-2004.
XX
PF 29-OCT-2003; 2003WO-US034598.
XX
PR 31-OCT-2002; 2002US-00286581.
XX
PA (GLAD-) GLADSTONE INST J DAVID.
XX
PI Cases S, Stone SJ, Zhou P, Farese RV, Yen CE;
XX
DR WPI; 2004-400668/37.
XX
PT New mammalian monoacylglycerol acyltransferase 2 polypeptide, useful for
PT treating cardiovascular disease, hyperlipidemia, obesity, diabetes,
PT cancer, neurological disorders and immunological disorders.
XX
PS Disclosure; SEQ ID NO 18; 98pp; English.
XX
CC The present invention describes a mammalian monoacylglycerol
CC acyltransferase (MGAT, EC 2.3.1.22) polypeptide (Ia) and a diacylglycerol
CC transferase (DGAT, EC 2.3.1.20) polypeptide (Ib) present in other than
CC its naturally occurring environment. Also described: (1) a mammalian
CC polynucleotide (II) present in other than its natural environment
CC encoding a polypeptide that exhibits MGAT and/or DGAT activity; (2) an
CC expression cassette (III) comprising a transcriptional initiation region
CC functional in an expression host, (II) under the transcriptional
CC regulation of the transcriptional initiation region, and transcriptional
CC termination region functional in the expression host; (3) a cell (IV)
CC comprising (III) as a part of an extrachromosomal element or integrated
CC into the genome of a host cell as a result of introducing (III) into the
CC host cell; (4) cellular progeny (V) of (IV); (5) preparing (Ia) and/or
CC (Ib); (6) monoclonal antibody (VI) binding specifically to (Ia) or (Ib);
CC (7) inhibiting (M1) the activity of (Ia) or (Ib); and (8) identifying an
CC agent that inhibits an acyltransferase activity of MGAT2 polypeptide.
CC (Ia) and (Ib) have cardiovascular, anorectic, antilipaemic, antidiabetic,
CC cytostatic and neuroprotective activities. (Ia) can be used for producing
CC in vitro models of diglyceride and/or triglyceride synthesis, and for
CC producing triglyceride compositions which find use in foodstuffs,
CC spreads, cooking materials, feedstocks and in industries for producing
CC chemicals, lubricants and surfactants. (Ia), (Ib) and (VI) are useful for
CC treating disease conditions associated with acylglycerol metabolism,
CC particularly associated with diacylglycerol O-acyltransferase 2 alpha
CC (DGAT2alpha), MGAT1 or MGAT2 activity. The disease conditions include
CC cardiovascular disease, hyperlipidaemia, obesity, diabetes, cancer,
CC neurological disorders and immunological disorders. (II) can be in gene
CC therapy to treat disorders associated with DGAT2alpha, MGAT1 or MGAT2
CC defects, as probes and primers in hybridisation applications (e.g., PCR),
CC for identifying expression patterns in biological specimens, for
CC preparing cell or animal models for DGAT2alpha, MGAT1 or MGAT2 function,
CC for preparing in vitro models for (DGAT2alpha), MGAT1 or MGAT2 function,
CC to generate transgenic host. The present sequence represents a human
CC acylglycerol acyltransferase related nucleotide sequence, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 1233 BP; 259 A; 360 C; 342 G; 272 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 705 GCATTGCCACTCCCATTCTT 686

RESULT 22
AAZ33556/c
ID AAZ33556 standard; cDNA; 1303 BP.
XX
AC AAZ33556;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human breast tumour-associated EST 16.
XX
KW Expressed sequence tag; EST; human; breast; cancer; cytostatic;
KW medicaments; gene therapy; treatment; fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19813835-A1.
XX
PD 23-SEP-1999.
XX
PF 20-MAR-1998; 98DE-01013835.
XX
PR 20-MAR-1998; 98DE-01013835.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX
DR WPI; 1999-528979/45.
DR P-PSDB; AAY48474.
XX
PT Human nucleic acid sequences and protein products from normal breast
PT tissue, useful for breast cancer therapy.
XX
PS Claim 1a; 103; 206pp; German.
XX
CC This invention describes novel human nucleic acid sequences from normal
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer and for treating illnesses associated with
CC fat metabolism. AAZ33541-Z33610 represent expressed sequence tags
CC described in the method of the invention
XX
SQ Sequence 1303 BP; 292 A; 337 C; 352 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 151 GCATTGCCACTCCCATTCTT 132

RESULT 23
ADR26804
ID ADR26804 standard; DNA; 1510 BP.
XX
AC ADR26804;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #2665.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX

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PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ,  He Y;
XX
DR   WPI; 2004-593473/57.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 2665; 226pp; English.
XX
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 1510 BP; 375 A; 398 C; 393 G; 344 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 13;  Length 1510;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       1491 GCATTGCCACTCCCATTCTT 1510


RESULT 24
ABL53628/c
ID   ABL53628 standard; cDNA; 1543 BP.
XX
AC   ABL53628;
XX
DT   17-JUN-2002  (first entry)
XX
DE   Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.
XX
KW   BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;
KW   cytostatic; differential expression; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             228. .1394
FT                   /*tag=  a
FT                   /product= "BSTP-ECG1"
XX
PN   WO200208260-A2.
XX
PD   31-JAN-2002.
XX
PF   26-JUL-2001; 2001WO-US023439.
XX
PR   26-JUL-2000; 2000US-0220967P.
PR   06-DEC-2000; 2000US-0251669P.
XX
PA   (STRD ) UNIV STANFORD.
PA   (GENO-) APPLIED GENOMICS INC.
XX
PI   Botstein D,  Brown PO,  Perou C,  Ross D,  Seitz R;
XX
DR   WPI; 2002-315251/35.
DR   P-PSDB; ABB75677.
XX
PT   Novel substantially purified polypeptide encoded by breast protein-
PT   eukaryotic conserved gene 1, useful for diagnosing, treating or
PT   preventing breast cancer, and for classifying cancer.
XX
PS   Disclosure; Fig 1D; 127pp; English.
XX
CC   The present sequence is that of a BSTP-ECG1 (breast protein-eukaryotic
CC   conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see
CC   ABB75677). The cDNA corresponds to a 1.5 kb mRNA isoform detected in
CC   liver tumour-derived HepG2 cells (ATCC HB-8065), colon tumour-derived
CC   COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7
CC   cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BST-
CC   ECG1 mRNA are predicted resulting from alternative 3' processing. BSTP-
CC   ECG1 is differentially expressed among breast tumours, making it useful
CC   for the diagnosis, treatment, prevention, prognosis and classification of
CC   cancer, especially breast cancer, and a target for therapeutic
CC   intervention. The invention provides BSTP-ECG1 polypeptides and
CC   polynucleotides, expression vectors, host cells, antibodies, agonists and
CC   antagonists. It also provides methods for treating or preventing
CC   disorders of cell proliferation, particularly breast cancer, by
CC   administering a polypeptide, polynucleotide or antibody of the invention.
CC   Also provided are methods of classifying diseases, particularly breast
CC   cancer, by detecting expression of BSTP-ECG1 or a polynucleotide encoding
CC   it, and of providing diagnostic, prognostic and/or predictive information
CC   for a patient based on the detection and/or measurement of BSTP-ECG1 or a
CC   polynucleotide encoding BSTP-ECG1. Since BST-ECG1 mRNA can be detected in
CC   a variety of tumour-derived cell lines, these methods may also be
CC   applicable to additional tumour types
XX
SQ   Sequence 1543 BP; 321 A; 452 C; 441 G; 329 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 1543;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        925 GCATTGCCACTCCCATTCTT 906


RESULT 25
AAA37103/c
ID   AAA37103 standard; cDNA; 1570 BP.
XX
AC   AAA37103;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Human PRO1433 (UNQ738) cDNA sequence SEQ ID NO:291.
XX
KW   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW   transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200012708-A2.
XX
PD   09-MAR-2000.
XX
PF   01-SEP-1999;   99WO-US020111.
XX
PR   01-SEP-1998;   98US-0098716P.
PR   01-SEP-1998;   98US-0098749P.
PR   01-SEP-1998;   98US-0098750P.
PR   02-SEP-1998;   98US-0098803P.
PR   02-SEP-1998;   98US-0098821P.
PR   02-SEP-1998;   98US-0098843P.
PR   09-SEP-1998;   98US-0099536P.
PR   09-SEP-1998;   98US-0099596P.
PR   09-SEP-1998;   98US-0099598P.
PR   09-SEP-1998;   98US-0099602P.
PR   09-SEP-1998;   98US-0099642P.
PR   10-SEP-1998;   98US-0099741P.
PR   10-SEP-1998;   98US-0099754P.
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PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR P-PSDB; AAY99421.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS Claim 2; Fig 163; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 26
AAF54409/c

```
ID   AAF54409 standard; DNA; 1570 BP.
XX
AC   AAF54409;
XX
DT   02-APR-2001  (first entry)
XX
DE   Primer #86 used in the identification of proteins.
XX
KW   Secreted; transmembrane; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US004342.
XX
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020111.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   16-DEC-1999;   99WO-US030095.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy.
XX
PS   Example 84; Page 457; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of anti-
CC   sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents. The nucleic
CC   acids may also be used in gene therapy
XX
SQ   Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 27
AAS46092/c
ID   AAS46092 standard; cDNA; 1570 BP.
XX
AC   AAS46092;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human DNA encoding PRO polypeptide sequence #168.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW   PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006520.
XX
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   06-MAR-2000; 2000US-0186968P.
PR   14-MAR-2000; 2000US-0189320P.
PR   14-MAR-2000; 2000US-0189328P.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000US-0190828P.
PR   21-MAR-2000; 2000US-0191007P.
PR   21-MAR-2000; 2000US-0191048P.
PR   21-MAR-2000; 2000US-0191314P.
PR   28-MAR-2000; 2000US-0192655P.
PR   29-MAR-2000; 2000US-0193032P.
PR   29-MAR-2000; 2000US-0193053P.
PR   30-MAR-2000; 2000WO-US008439.
PR   04-APR-2000; 2000US-0194449P.
PR   04-APR-2000; 2000US-0194647P.
PR   11-APR-2000; 2000US-0195975P.
PR   11-APR-2000; 2000US-0196000P.
PR   11-APR-2000; 2000US-0196187P.
PR   11-APR-2000; 2000US-0196690P.
PR   11-APR-2000; 2000US-0196820P.
PR   18-APR-2000; 2000US-0198121P.
PR   18-APR-2000; 2000US-0198585P.
PR   25-APR-2000; 2000US-0199397P.
PR   25-APR-2000; 2000US-0199550P.
PR   25-APR-2000; 2000US-0199654P.
PR   03-MAY-2000; 2000US-0201516P.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   P-PSDB; AAU29191.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumors, such as prostate and breast tumors, in mammals and to
PT   screen for modulators of the compounds.
XX
PS   Claim 2; Fig 335; 774pp; English.
XX
CC   Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC   primers for PRO polypeptides of the invention. The sequences of the
CC   invention can be used to detect the presence of a tumour in a mammal by
CC   comparing the level of expression of a PRO polypeptide in a test sample
CC   of cells from the animal and a control sample of normal cells, whereby a
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CC   higher level of expression in the test sample indicates the presence of a
CC   tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC   pigs, goats and rabbits but are preferably human. The polypeptides can be
CC   used to stimulate tumour necrosis factor (TNF) alpha release from human
CC   blood, when contacted with it. A specific polypeptide can be used to
CC   stimulate the proliferation or differentiation of chondrocyte cells. The
CC   PRO proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders
XX
SQ   Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 28
ACA89542/c
ID   ACA89542 standard; cDNA; 1570 BP.
XX
AC   ACA89542;
XX
DT   09-JUL-2003  (first entry)
XX
DE   cDNA encoding human PRO polypeptide #168.
XX
KW   Human; PRO polypeptide; secreted protein; transmembrane protein;
KW   chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW   prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW   tumour necrosis factor-alpha; proliferation; differentiation;
KW   chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW   arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US2003036141-A1.
XX
PD   20-FEB-2003.
XX
PF   01-JUL-2002; 2002US-00187597.
XX
PR   18-SEP-1997;   97US-0059263P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 20; DB 8; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        882 GCATTGCCACTCCCATTCTT 863
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RESULT 29
ACA73552/c
ID ACA73552 standard; cDNA; 1570 BP.
XX
AC ACA73552;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #168.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036146-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187603.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
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PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332034/31.
DR P-PSDB; ABU86360.
XX
PT Three hundred and five nucleic acids encoding PRO polypeptides, useful in
PT gene therapy, chromosome identification, tissue typing, and for detecting
PT the presence of tumor in a mammal.
XX
PS Claim 2; Fig 335; 707pp; English.
XX
CC The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
CC them, or encoding a PRO polypeptide lacking its associated signal peptide
CC or an extracellular domain of the PRO polypeptide, with or lacking its
CC associated signal peptide. Also included are the encoded PRO proteins,
CC PRO expression vectors, host cells transformed with the vector (used to
CC produce PRO proteins), a chimaeric molecule comprising the PRO
CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, a method for stimulating the release of tumor necrosis factor
CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,
CC PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
CC PRO4333), a method for stimulating the proliferation or differentiation
CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a cDNA encoding a PRO
CC protein
XX
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 30
ACA05867/c
ID ACA05867 standard; cDNA; 1570 BP.
XX
AC ACA05867;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #168.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
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PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
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PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.
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PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
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PR 28-FEB-2001; 2001WO-US006520.
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PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
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PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332039/31.
DR P-PSDB; ABU67573.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.
XX
PS Claim 2; Fig 335; 706pp; English.
XX
CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 31
ACA66701/c
ID ACA66701 standard; cDNA; 1570 BP.
XX
AC ACA66701;
XX
DT 23-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO protein #168.
XX
KW Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
KW liver; PRO; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036137-A1.
XX
PD 20-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184640.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
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XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-342038/32.
DR P-PSDB; ABU80601.
XX
PT Three hundred and five nucleic acids encoding secreted and transmembrane
PT PRO polypeptides, useful for the diagnosis, prevention and/or treatment
PT of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
PT cervical or liver tumors.
XX
PS Claim 2; Fig 335; 708pp; English.
XX
CC The invention relates to three hundred and five nucleic acids encoding
CC PRO polypeptides (secreted and transmembrane). Methods and compositions
CC of the present invention are useful for the diagnosis, prevention and/or
CC treatment of tumours, such as adrenal, lung, colon, breast, prostate,
CC rectal, cervical or liver tumours. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The present
CC sequence represents a cDNA encoding a human PRO polypeptide of the
CC invention
XX
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 882 GCATTGCCACTCCCATTCTT 863

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AC ACF20276;
XX
DT 18-SEP-2003 (first entry)
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KW KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040063-A1.
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RESULT 33
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ID ACF19662 standard; cDNA; 1570 BP.
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AC ACF19662;
XX
DT 17-SEP-2003 (first entry)
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DE Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040064-A1.
XX
PD 27-FEB-2003.

XX
PF 26-JUN-2002; 2002US-00183008.
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PR 18-SEP-1997; 97US-0059263P.
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DT 25-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
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XX
PD 06-FEB-2003.
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KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
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KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 882 GCATTGCCACTCCCATTCTT 863

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ID ACF00267 standard; cDNA; 1570 BP.
XX
AC ACF00267;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted polypeptide PRO1433-encoding cDNA, SEQ ID NO:335.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054474-A1.
XX
PD 20-MAR-2003.
XX
PF 22-JUL-2002; 2002US-00201530.
XX
PR 22-JUN-1998; 98US-0090254P.
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PR 25-AUG-1999; 99US-00380137.
PR 28-FEB-2001; 2001WO-US006520.
PR 15-JAN-2002; 2002US-00052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-503631/47.
DR P-PSDB; ABR78394.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, or for preparing a medicament for treating a condition
PT that is responsive to the PRO polypeptide or anti-PRO antibody.
XX
PS Claim 2; Fig 335; 700pp; English.
XX
CC The invention relates to human PRO secreted/transmembrane polypeptides
CC (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The
CC invention also relates to sequences at least 80% identical to the PRO
CC nucleic acid and polypeptide sequences of the invention, recombinant
CC vectors and host cells comprising a PRO nucleic acid, a method for the

CC recombinant production of a PRO polypeptide, antibodies against a PRO
CC polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic
CC acids encoding PRO polypeptides of the invention were initially
CC identified via homology screening using consensus sequences based on the
CC extracellular domain sequences from known secreted proteins. Human cDNA
CC libraries containing sequences of interest were identified using
CC oligonucleotides based on the consensus sequences, and cDNA clones were
CC isolated and characterised. The PRO polypeptides are useful for
CC stimulating release of tumour necrosis factor-alpha (TNF-alpha) from
CC human blood and may thus be used in the treatment of conditions in which
CC enhanced TNF-alpha release would be beneficial. They are also useful for
CC stimulating the proliferation or differentiation of chondrocytes and as
CC such may be used in the treatment of various bone and/or cartilage
CC disorders such as arthritis and sports injuries. The PRO polypeptides may
CC be used in a method for detecting the presence of a tumour (e.g., an
CC adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
CC tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
CC method involves comparing the level of expression of the PRO polypeptide
CC in test and control samples, where a higher level of expression of PRO
CC polypeptide in the test sample as compared to the control sample is
CC indicative of the presence of a tumour. The PRO polypeptides are
CC additionally useful for in drug screening to identify agonists and
CC antagonists of PRO polypeptides. PRO nucleic acids are useful as
CC hybridisation probes (for isolation of cDNA molecules), in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA and in gene
CC therapy. The nucleic acids can also be used for mapping genes encoding
CC PRO polypeptides, for genetic analysis of individuals with genetic
CC disorders, and for generating either transgenic animals or knock-out
CC animals which are useful in the development and screening of
CC therapeutically useful compounds. Sequences ACF00100-00404 represent
CC cDNAs encoding the human PRO secreted/transmembrane polypeptides of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1570 BP; 391 A; 435 C; 425 G; 319 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 38
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ID ACA72324 standard; cDNA; 1570 BP.
XX
AC ACA72324;
XX
DT 30-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1433 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
KW chondrocyte stimulator; chromosome mapping; gene mapping;
KW transgenic animal; knock-out animal; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032114-A1.
XX
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176919.
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PR 02-OCT-1998; 98US-0102965P.
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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        882 GCATTGCCACTCCCATTCTT 863
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RESULT 39
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ID ACD04848 standard; cDNA; 1570 BP.
XX
AC ACD04848;
XX
DT 06-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1433 cDNA.
XX
KW Human; ss; gene therapy; tumour necrosis factor alpha; TNF-alpha;
KW chondrocyte stimulation; tumour; tissue typing; gene.
XX
OS Homo sapiens.
XX
PN US2003032101-A1.
XX
PD 13-FEB-2003.
XX
PF 17-JUN-2002; 2002US-00173695.
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KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
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KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
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KW chondrocyte proliferation; chondrocyte differentiation; tumour detection;
KW tissue typing; gene.
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OS Homo sapiens.
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ID ACA70192 standard; cDNA; 1570 BP.
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DT 11-AUG-2003 (first entry)
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KW Human; gene; ss; secreted and transmembrane protein; PRO;
KW chromosome mapping; gene mapping; gene therapy;
KW tumour necrosis factor alpha; TNF-alpha; chondrocyte; tumour.
XX
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KW   transgenic animal; knockout animal; tissue typing;
KW   chondrocyte proliferation; chondrocyte differentiation;
KW   tumour necrosis factor-alpha stimulation; TNF-alpha stimulation; gene;
KW   ss.
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KW   bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW   adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW   liver; drug screening; transgenic animal; genetic analysis;
KW   antiarthritic; vulnerary; gene therapy; gene; ss.
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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	827	6	BD218489	BD218489 Diacylgly
c 2	20	100.0	885	6	BD218493	BD218493 Diacylgly
c 3	20	100.0	933	4	AY675174	AY675174 Bos tauru
c 4	20	100.0	1158	6	CQ723322	CQ723322 Sequence
c 5	20	100.0	1167	6	AX430068	AX430068 Sequence
c 6	20	100.0	1233	9	AF384161	AF384161 Homo sapi
c 7	20	100.0	1304	6	BD135168	BD135168 Human nuc
c 8	20	100.0	1304	6	AX017478	AX017478 Sequence
c 9	20	100.0	1330	10	AF384160	AF384160 Mus muscu
c 10	20	100.0	1433	4	BTA519787	AJ519787 Bos tauru
c 11	20	100.0	1543	6	AX430070	AX430070 Sequence
c 12	20	100.0	1554	9	BC015234	BC015234 Homo sapi
c 13	20	100.0	1570	6	AX376268	AX376268 Sequence
c 14	20	100.0	1570	6	AX697223	AX697223 Sequence
c 15	20	100.0	1570	9	AY358532	AY358532 Homo sapi
c 16	20	100.0	1735	9	AK074203	AK074203 Homo sapi
c 17	20	100.0	2009	9	AB073384	AB073384 Homo sapi
c 18	20	100.0	2075	6	CQ498467	CQ498467 Sequence
c 19	20	100.0	2263	10	BC043447	BC043447 Mus muscu
c 20	20	100.0	2364	9	HSM805323	AL834287 Homo sapi
c 21	20	100.0	2398	6	AX281630	AX281630 Sequence
c 22	20	100.0	2418	6	AX430071	AX430071 Sequence
c 23	20	100.0	2439	6	BD181466	BD181466 A gene of
c 24	20	100.0	2439	9	AB048286	AB048286 Homo sapi
c 25	20	100.0	2445	6	AX430069	AX430069 Sequence
c 26	20	100.0	2678	6	AX747231	AX747231 Sequence
c 27	20	100.0	2678	9	AK091870	AK091870 Homo sapi
c 28	20	100.0	2713	6	BD181467	BD181467 A gene of
c 29	20	100.0	2788	4	BTA534371	AJ534371 Bos tauru
c 30	20	100.0	95585	9	AP003031	AP003031 Homo sapi
c 31	20	100.0	146346	2	AC111120	AC111120 Mus muscu
c 32	20	100.0	155227	2	AC115850	AC115850 Mus muscu
33	20	100.0	162719	2	AC021221	AC021221 Homo sapi
c 34	19	95.0	721	4	AY589091S2	AY589092 Bos tauru
35	17	85.0	10013	1	AE004034	AE004034 Xylella f
c 36	17	85.0	43593	9	AL954659	AL954659 Human DNA
37	17	85.0	69294	2	AC100360	AC100360 Mus muscu
c 38	17	85.0	98637	2	AL365359	AL365359 Homo sapi
39	17	85.0	104695	9	HSDJ961O8	AL121879 Human DNA
40	17	85.0	110000	2	AC130947_2	Continuation (3 of
41	17	85.0	143454	2	AC026820	AC026820 Homo sapi
42	17	85.0	156149	2	AC027556	AC027556 Homo sapi
43	17	85.0	165910	9	AL928688	AL928688 Human DNA
44	17	85.0	166004	9	AL935036	AL935036 Human DNA
45	17	85.0	167099	9	AL161734	AL161734 Human DNA
c 46	17	85.0	176733	9	AC092850	AC092850 Homo sapi
47	17	85.0	179881	2	AL356978	AL356978 Homo sapi
48	17	85.0	184485	2	AL445525	AL445525 Mus muscu
c 49	17	85.0	192053	9	AC090155	AC090155 Homo sapi
c 50	17	85.0	211039	2	AC068555	AC068555 Homo sapi
51	17	85.0	216423	2	BX928749	BX928749 Danio rer
c 52	17	85.0	219476	9	AC068945	AC068945 Homo sapi
53	17	85.0	221126	2	AC021184	AC021184 Homo sapi
c 54	17	85.0	225606	2	AC122078	AC122078 Rattus no
c 55	17	85.0	242247	2	AC133695	AC133695 Rattus no
56	17	85.0	300775	1	AE012557	AE012557 Xylella f
57	17	85.0	316704	9	AF239258S3	AF223391 Homo sapi
58	17	85.0	345682	2	AC095142	AC095142 Rattus no
c 59	16	80.0	616	6	AR563384	AR563384 Sequence
60	16	80.0	1407	1	AY204396	AY204396 Leptospir
61	16	80.0	4526	9	HSAENAC1	AF060910 Homo sapi
c 62	16	80.0	5308	5	BC068777	BC068777 Xenopus l
c 63	16	80.0	14328	6	CQ575480	CQ575480 Sequence
64	16	80.0	40400	2	AC012915	AC012915 Drosophil
65	16	80.0	55238	2	AC013422	AC013422 Drosophil
66	16	80.0	58328	2	AC019967	AC019967 Drosophil
67	16	80.0	64952	9	AL359745	AL359745 Human DNA
68	16	80.0	68531	2	AC055868	AC055868 Homo sapi
c 69	16	80.0	97837	2	AC151676	AC151676 Gallus ga
70	16	80.0	108100	9	AC103881	AC103881 Homo sapi
71	16	80.0	110000	2	AC147965_0	AC147965 Gallus ga
72	16	80.0	110000	10	AE014173_2	Continuation (3 of
c 73	16	80.0	127946	8	AC104473	AC104473 Oryza sat
74	16	80.0	128559	8	CNS08C8I	AL731878 Oryza sat
75	16	80.0	130965	9	AC026773	AC026773 Homo sapi
76	16	80.0	133759	8	OSJN00289	AL731642 Oryza sat
77	16	80.0	136393	2	AC151700	AC151700 Gallus ga
78	16	80.0	140026	9	AC005840	AC005840 Homo sapi
79	16	80.0	140070	2	AC142487	AC142487 Rattus no
c 80	16	80.0	142772	8	AP004184	AP004184 Oryza sat
81	16	80.0	142772	10	AL928683	AL928683 Mouse DNA
c 82	16	80.0	143046	8	AP004191	AP004191 Oryza sat
c 83	16	80.0	144563	8	CNS08C7P	AL731740 Oryza sat
c 84	16	80.0	150137	8	AC135226	AC135226 Oryza sat
85	16	80.0	152884	9	AC138625	AC138625 Homo sapi
c 86	16	80.0	154729	2	AC138879	AC138879 Homo sapi
87	16	80.0	157462	9	AC130459	AC130459 Homo sapi
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89	16	80.0	158420	9	AC137788	AC137788 Homo sapi
90	16	80.0	159832	2	AC110764	AC110764 Homo sapi
91	16	80.0	161117	3	AC008311	AC008311 Drosophil
c 92	16	80.0	163384	9	AC026409	AC026409 Homo sapi

	93	16	80.0	163631	9	AC009276	AC009276 Homo sapi
c	94	16	80.0	170919	9	AC078847	AC078847 Homo sapi
c	95	16	80.0	172266	3	AC092190	AC092190 Drosophil
c	96	16	80.0	173404	10	AC114559	AC114559 Mus muscu
c	97	16	80.0	173906	2	AC034171	AC034171 Homo sapi
	98	16	80.0	175099	9	AC109135	AC109135 Homo sapi
	99	16	80.0	175158	2	AC120531	AC120531 Oryza sat
c	100	16	80.0	176981	9	AC136634	AC136634 Homo sapi

ALIGNMENTS

```
RESULT 1
BD218489/c
LOCUS       BD218489                827 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Diacylglycerol acyl transferase proteins.
ACCESSION   BD218489
VERSION     BD218489.1  GI:33028259
KEYWORDS    JP 2002519051-A/30.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Lardizabal,K.D., Hawkins,D. and Thompson,G.A.
  TITLE     Diacylglycerol acyl transferase proteins
  JOURNAL   Patent: JP 2002519051-A 30 02-JUL-2002;
            CALGENE LLC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519051-A/30
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000558114
            PR   02-JUL-1998 US    60/091631,23-APR-1999 US    60/130829 PI
            KATHRYN DENNIS LARDIZABAL,DEBORAH HAWKINS,GREGORY A THOMPSON PC
            C12N15/09,A01H5/00,A61K45/00,A61P3/04,A61P3/06,A61P3/10 PC
            ,A61P9/00,A61P35/00,
            PC   C07K16/40,C12N5/10,C12N9/10//(C12N9/10,C12R1:66,C12R1:865), PC
              C12N15/00,
            PC   C12N5/00
            CC   Diacylglycerol acyl transferase proteins
            FH   Key             Location/Qualifiers
            FT   source          1. .827
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .827
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        479 GCATTGCCACTCCCATTCTT 460


RESULT 2
BD218493/c
LOCUS       BD218493                885 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Diacylglycerol acyl transferase proteins.
ACCESSION   BD218493
VERSION     BD218493.1  GI:33028263
KEYWORDS    JP 2002519051-A/34.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Lardizabal,K.D., Hawkins,D. and Thompson,G.A.
  TITLE     Diacylglycerol acyl transferase proteins
  JOURNAL   Patent: JP 2002519051-A 34 02-JUL-2002;
            CALGENE LLC
COMMENT     OS   Mus sp. (murine)
            PN   JP 2002519051-A/34
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000558114
            PR   02-JUL-1998 US    60/091631,23-APR-1999 US    60/130829 PI
            KATHRYN DENNIS LARDIZABAL,DEBORAH HAWKINS,GREGORY A THOMPSON PC
            C12N15/09,A01H5/00,A61K45/00,A61P3/04,A61P3/06,A61P3/10 PC
            ,A61P9/00,A61P35/00,
            PC   C07K16/40,C12N5/10,C12N9/10//(C12N9/10,C12R1:66,C12R1:865), PC
              C12N15/00,
            PC   C12N5/00
            CC   unsure at all n locations
            FH   Key             Location/Qualifiers
            FT   unsure          (1). .(885).
FEATURES             Location/Qualifiers
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                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 885;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
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Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        482 GCATTGCCACTCCCATTCTT 463


RESULT 3
AY675174/c
LOCUS       AY675174                933 bp    mRNA    linear   MAM 28-JUL-2004
DEFINITION  Bos taurus DGAT2 mRNA, partial cds.
ACCESSION   AY675174
VERSION     AY675174.1  GI:50541688
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   Xu,X.R. and Xu,S.Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2004) Institute of Animal Science, Academic of
            Agriculture Science of China, Haidian District, Beijing 100094,
            China
FEATURES             Location/Qualifiers
     source          1. .933
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
     CDS             <1. .812
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                     /product="DGAT2"
                     /protein_id="AAT78344.1"
                     /db_xref="GI:50541689"
                     /translation="GGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTSRNYIFGYHPH
                     GIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVNRDTI
                     DYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPTYSF
                     GENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPITTV
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ORIGIN

  Query Match            100.0%;  Score 20;  DB 4;  Length 933;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        343 GCATTGCCACTCCCATTCTT 324


RESULT 4
CQ723322/c
LOCUS       CQ723322               1158 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 9256 from Patent WO02068579.
ACCESSION   CQ723322
VERSION     CQ723322.1  GI:42284179
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 9256 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1158
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 5
AX430068/c
LOCUS       AX430068               1167 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 2 from Patent WO0208260.
ACCESSION   AX430068
VERSION     AX430068.1  GI:21541216
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R.
  TITLE     Bstp-ecg1 protein and related reagents and methods of use thereof
  JOURNAL   Patent: WO 0208260-A 2 31-JAN-2002;
            STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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                     /note="Nucleotide sequence of an open reading frame that
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ORIGIN

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Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 6
AF384161/c
LOCUS       AF384161               1233 bp    mRNA    linear   PRI 11-JAN-2002
DEFINITION  Homo sapiens diacylglycerol acyltransferase 2 mRNA, complete cds.
ACCESSION   AF384161
VERSION     AF384161.2  GI:18129608
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1233)
  AUTHORS   Cases,S., Stone,S.J., Zhou,P., Yen,E., Tow,B., Lardizabal,K.D.,
            Voelker,T. and Farese,R.V. Jr.
  TITLE     Cloning of DGAT2, a second mammalian diacylglycerol
            acyltransferase, and related family members
  JOURNAL   J. Biol. Chem. 276 (42), 38870-38876 (2001)
  MEDLINE   21486408
   PUBMED   11481335
REFERENCE   2  (bases 1 to 1233)
  AUTHORS   Cases,S., Stone,S., Zhou,P. and Farese,R.V. Jr.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2001) Gladstone Institutes, 2550 23rd Street, San
            Francisco, CA 94110, USA
COMMENT     On Jan 11, 2002 this sequence version replaced gi:15099952.
FEATURES             Location/Qualifiers
     source          1. .1233
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="testis"
     CDS             8. .1174
                     /note="DGAT-2"
                     /codon_start=1
                     /product="diacylglycerol acyltransferase 2"
                     /protein_id="AAK84176.2"
                     /db_xref="GI:18129609"
                     /translation="MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGS
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                     HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVSR
                     DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPI
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 1233;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        705 GCATTGCCACTCCCATTCTT 686


RESULT 7
BD135168/c
LOCUS       BD135168               1304 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Human nucleic acid sequence originating in normal mammary tissue.
ACCESSION   BD135168
VERSION     BD135168.1  GI:23230113
KEYWORDS    JP 2002506639-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1304)
  AUTHORS   Speft,T., Hintzman,B., Shcmitt,A., Pirarski,C., Duhl,E. and
            Rosenthal,A.
  TITLE     Human nucleic acid sequence originating in normal mammary tissue
  JOURNAL   Patent: JP 2002506639-A 15 05-MAR-2002;
            METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002506639-A/15
            PD   05-MAR-2002
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            PF   19-MAR-1999 JP 2000536838
            PR   20-MAR-1998 DE 198 13 835.0
            PI   THOMAS SPEFT,BERND HINTZMAN,ARMIN SHCMITT,CHRISTIAN PIRARSKI,
            PI   EDGAR DUHL,
            PI   ANDRE ROSENTHAL
            PC   C12N15/09,A61K48/00,A61P35/00,A61P43/00,A61P43/00,C07K14/47,
            PC   C07K16/18,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//A61K38/00, PC
             C12N15/00,
            PC   C12N5/00,A61K37/02
            CC   Human nucleic acid sequence originating in normal mammary  CC
                 tissue
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        151 GCATTGCCACTCCCATTCTT 132


RESULT 8
AX017478/c
LOCUS       AX017478                1304 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 21 from Patent WO9947655.
ACCESSION   AX017478
VERSION     AX017478.1  GI:10042275
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
            Pilarsky,C.
  TITLE     Human nucleic acid sequences from normal breast tissue
  JOURNAL   Patent: WO 9947655-A 21 23-SEP-1999;
            SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
            BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
            (DE); PILARSKY CHRISTIAN (DE)
FEATURES             Location/Qualifiers
     source          1. .1304
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1304;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        151 GCATTGCCACTCCCATTCTT 132


RESULT 9
AF384160/c
LOCUS       AF384160                1330 bp    mRNA    linear   ROD 16-OCT-2001
DEFINITION  Mus musculus diacylglycerol acyltransferase 2 mRNA, complete cds.
ACCESSION   AF384160
VERSION     AF384160.1  GI:15099950
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1330)
  AUTHORS   Cases,S., Stone,S.J., Zhou,P., Yen,E., Tow,B., Lardizabal,K.D.,
            Voelker,T. and Farese,R.V. Jr.
  TITLE     Cloning of DGAT2, a second mammalian diacylglycerol
            acyltransferase, and related family members
  JOURNAL   J. Biol. Chem. 276 (42), 38870-38876 (2001)
  MEDLINE   21486408
   PUBMED   11481335
REFERENCE   2  (bases 1 to 1330)
  AUTHORS   Cases,S., Stone,S., Zhou,P. and Farese,R.V. Jr.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2001) Gladstone Institutes, 2550 23rd Street, San
            Francisco, CA 94110, USA
FEATURES             Location/Qualifiers
     source          1. .1330
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="liver"
     CDS             60. .1226
                     /note="DGAT-2"
                     /codon_start=1
                     /product="diacylglycerol acyltransferase 2"
                     /protein_id="AAK84175.1"
                     /db_xref="GI:15099951"
                     /translation="MKTLIAAYSGVLRGERRAEAARSENKNKGSALSREGSGRWGTGS
                     SILSALQDIFSVTWLNRSKVEKQLQVISVLQWVLSFLVLGVACSVILMYTFCTDCWLI
                     AVLYFTWLAFDWNTPKKGGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGY
                     HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVNR
                     DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLKNRKGFVKLALRHGADLVPT
                     YSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPI
                     TTVVGEPITVPKLEHPTQKDIDLYHAMYMEALVKLFDNHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 1330;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        757 GCATTGCCACTCCCATTCTT 738


RESULT 10
BTA519787/c
LOCUS       BTA519787               1433 bp    mRNA    linear   MAM 06-FEB-2004
DEFINITION  Bos taurus mRNA for putative diacylglycerol O-acyltransferase
            (DGAT2 gene).
ACCESSION   AJ519787
VERSION     AJ519787.1  GI:42454646
KEYWORDS    DGAT2 gene; diacylglycerol O-acyltransferase 2 protein.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 1433)
  AUTHORS   Winter,A., can Eckveld,M., Bininda Emonds,O.R.P., Habermann,F.A.
            and Fries,R.
  TITLE     Genomic organization of the dgat2/mogat gene family in cattle (bos
            taurus) and other mammals
  JOURNAL   (er) Cytogenet. Genome Res. 102: DOI, 10.1159/000075723 (2003)
REFERENCE   2  (bases 1 to 1433)
  AUTHORS   Winter,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2002) Lehrstuhl fuer Tierzucht, Technischen
            Universitaet Muenchen, Alte Akademie 12, Freising-Weihenstephan
            85354, GERMANY
FEATURES             Location/Qualifiers
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                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
     gene            1. .1433
                     /gene="DGAT2"
     CDS             199. .1284
                     /gene="DGAT2"
                     /codon_start=1
                     /product="putative diacylglycerol O-acyltransferase"
                     /protein_id="CAD58592.1"
                     /db_xref="GI:42454647"
                     /translation="MKTLIAAYSGVLRGTGSSILSALQDLFSVTWLNRAKVEKQLQVI
                     SVLQWVLSFLVLGVACSVILMYTFCTDCWLIAVLYFTWLVFDWNTPKKGGRRSQWVRN
                     WAVWRYFRDYFPIQLVKTHNLLTSRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPG
                     IRPYLATLAGNFRMPVLREYLMSGGICPVNRDTIDYLLSKNGSGNAIIIVVGGAAESL
                     SSMPGKNAVTLRNRKGFVKLALRHGADLVPTYSFGENEVYKQVIFEEGSWGRWVQKKF
                     QKYIGFAPCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPRLERPTQQDIDLYHAM
                     YVQALVKLFDQHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 1433;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        815 GCATTGCCACTCCCATTCTT 796


RESULT 11
AX430070/c
LOCUS       AX430070                1543 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 4 from Patent WO0208260.
ACCESSION   AX430070
VERSION     AX430070.1  GI:21541218
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R.
  TITLE     Bstp-ecg1 protein and related reagents and methods of use thereof
  JOURNAL   Patent: WO 0208260-A 4 31-JAN-2002;
            STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1543
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleotide sequence of a second cDNA that encodes
                     BSTP-ECG1"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1543;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        925 GCATTGCCACTCCCATTCTT 906


RESULT 12
BC015234/c
LOCUS       BC015234                1554 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens diacylglycerol O-acyltransferase homolog 2 (mouse),
            mRNA (cDNA clone MGC:17861 IMAGE:3903313), complete cds.
ACCESSION   BC015234
VERSION     BC015234.1  GI:15929601
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1554)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1554)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 22 Row: g Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 26024196.
FEATURES             Location/Qualifiers
     source          1. .1554
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:17861 IMAGE:3903313"
                     /tissue_type="Pancreas, epithelioid carcinoma"
                     /clone_lib="NIH_MGC_70"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .1554
                     /gene="DGAT2"
                     /db_xref="LocusID:84649"
                     /db_xref="MIM:606983"
     CDS             249. .1415
                     /gene="DGAT2"
                     /codon_start=1
                     /product="diacylglycerol O-acyltransferase homolog 2"
                     /protein_id="AAH15234.1"
                     /db_xref="GI:15929602"
                     /db_xref="LocusID:84649"
                     /db_xref="MIM:606983"
                     /translation="MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGS
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                    HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVSR
                    DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPI
                    YSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPI
                    TTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 1554;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        946 GCATTGCCACTCCCATTCTT 927


RESULT 13
AX376268/c
LOCUS       AX376268               1570 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 335 from Patent WO0168848.
ACCESSION   AX376268
VERSION     AX376268.1  GI:19170525
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0168848-A 335 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1570
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 14
AX697223/c
LOCUS       AX697223               1570 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 291 from Patent WO0078961.
ACCESSION   AX697223
VERSION     AX697223.1  GI:29498159
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
            Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
            Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0078961-A 291 28-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1570
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 15
AY358532/c
LOCUS       AY358532               1570 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA71184 DGAT2 (UNQ738) mRNA, complete cds.
ACCESSION   AY358532
VERSION     AY358532.1  GI:37182186
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1570)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1570)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1570
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA71184"
     gene            1. .1570
                     /locus_tag="UNQ738"
     CDS             185. .1351
                     /locus_tag="UNQ738"
                     /note="PRO1433"
                     /codon_start=1
                     /product="DGAT2"
                     /protein_id="AAQ88896.1"
                     /db_xref="GI:37182187"
                     /translation="MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGS
                     SILSALQDLFSVTWLNRSKVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI
                     AVLYFTWLVFDWNTPKKGGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGY
                     HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVSR
                     DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPI
                     YSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPI
                     TTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 16
AK074203/c
LOCUS       AK074203               1735 bp    mRNA    linear   PRI 12-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ23623 fis, clone ADSE01532.
ACCESSION   AK074203
VERSION     AK074203.1  GI:18676740
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
            Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
            Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
            Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
            Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1735)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Laboratory of Genome Structure, Human Genome
            Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
            (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
            Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing: Departent of Virology and Human
            Genome Center, Institute of Medical Science, University of Tokyo
            (partly supported by Science and Technology Agency).
FEATURES             Location/Qualifiers
     source          1. .1735
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADSE01532"
                     /tissue_type="adipose tissue"
                     /clone_lib="ad"
                     /note="cloning vector: pME18SFL3"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 1735;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        222 GCATTGCCACTCCCATTCTT 203


RESULT 17
AB073384/c
LOCUS       AB073384               2009 bp    mRNA    linear   PRI 26-AUG-2004
DEFINITION  Homo sapiens infant liver cDNA, clone:HMFN1045, full insert
            sequence.
ACCESSION   AB073384
VERSION     AB073384.1  GI:51555755
KEYWORDS    FLI_CDNA; oligo capping.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yamada,S., Ohira,M., Horie,H., Ando,K., Takayasu,H., Suzuki,Y.,
            Sugano,S., Hirata,T., Goto,T., Matsunaga,T., Hiyama,E., Hayashi,Y.,
            Ando,H., Suita,S., Kaneko,M., Sasaki,F., Hashizume,K., Ohnuma,N.
            and Nakagawara,A.
  TITLE     Expression profiling and differential screening between
            hepatoblastomas and the corresponding normal livers: identification
            of high expression of the PLK1 oncogene as a poor-prognostic
            indicator of hepatoblastomas
  JOURNAL   Oncogene 23 (35), 5901-5911 (2004)
  PUBMED    15221005
REFERENCE   2  (bases 1 to 2009)
  AUTHORS   Nakagawara,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2001) Akira Nakagawara, Chiba Cancer Center
            Research Institute, Division of Biochemistry; 666-2, Nitona-cho,
            Chuoh-ku, Chiba, Chiba 260-8717, Japan
            (E-mail:akiranak@chiba-ccri.chuo.chiba.jp,
            Tel:81-43-264-5431(ex.5201), Fax:81-43-262-8680)
FEATURES             Location/Qualifiers
     source          1. .2009
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HMFN1045"
                     /clone_lib="HMFN, human normal infant liver oligo-capping
                     cDNA library"
     gene            1. .2009
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     CDS             81. .974
                     /gene="HMFN1045"
                     /codon_start=1
                     /product="putative protein product of HMFN1045"
                     /protein_id="BAD38635.1"
                     /db_xref="GI:51555756"
                     /translation="MYIFCTDCWLIAVLYFTWLVFDWNTPKKGGRRSQWVRNWAVWRY
                     FRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLA
                     TLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGK
                     NAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGF
                     APCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALV
                     KLFDKHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 2009;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        505 GCATTGCCACTCCCATTCTT 486


RESULT 18
CQ498467/c
LOCUS       CQ498467               2075 bp    DNA     linear   PAT 30-JAN-2004
DEFINITION  Sequence 30334 from Patent WO0160860.
ACCESSION   CQ498467
VERSION     CQ498467.1  GI:41464103
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 30334 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2075
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 2075;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        938 GCATTGCCACTCCCATTCTT 919


RESULT 19
BC043447/c
LOCUS       BC043447               2263 bp    mRNA    linear   ROD 30-JUN-2004
DEFINITION  Mus musculus diacylglycerol O-acyltransferase 2, mRNA (cDNA clone
            MGC:49088 IMAGE:5125951), complete cds.
ACCESSION   BC043447
VERSION     BC043447.1  GI:27693971
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2263)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2263)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 86 Row: h Column: 12
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
     source          1. .2263
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="MGC:49088 IMAGE:5125951"
                     /tissue_type="Liver, normal. 5 month old male mouse."
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     gene            1. .2263
                     /gene="Dgat2"
                     /note="synonym: DGAT-2"
                     /db_xref="LocusID:67800"
                     /db_xref="MGI:1915050"
     CDS             202. .1368
                     /gene="Dgat2"
                     /codon_start=1
                     /product="diacylglycerol O-acyltransferase 2"
                     /protein_id="AAH43447.1"
                     /db_xref="GI:27693972"
                     /db_xref="LocusID:67800"
                     /db_xref="MGI:1915050"
                     /translation="MKTLIAAYSGVLRGERRAEAARSENKNKGSALSREGSGRWGTGS
                     SILSALQDIFSVTWLNRSKVEKQLQVISVLQWVLSFLVLGVACSVILMYTFCTDCWLI
                     AVLYFTWLAFDWNTPKKGGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGY
                     HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVNR
                     DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLKNRKGFVKLALRHGADLVPT
                     YSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPI
                     TTVVGEPITVPKLEHPTQKDIDLYHAMYMEALVKLFDNHKTKFGLPETEVLEVN"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 2263;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        899 GCATTGCCACTCCCATTCTT 880


RESULT 20
HSM805323/c
LOCUS       HSM805323              2364 bp    mRNA    linear   PRI 12-JUL-2002
DEFINITION  Homo sapiens mRNA; cDNA DKFZp667C1711 (from clone DKFZp667C1711).
ACCESSION   AL834287
VERSION     AL834287.1  GI:21739870
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2364)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp667C1711) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
     source          1. .2364
```

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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="RZPD:DKFZp667C1711"
                     /db_xref="taxon:9606"
                     /map="83.20 cR from top of Chr11 linkage group"
                     /clone="DKFZp667C1711"
                     /tissue_type="lymph node"
                     /clone_lib="667 (synonym: hlno2). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
     gene            1. .2364
                     /gene="DKFZp667C1711"
     CDS             <1. .1305
                     /gene="DKFZp667C1711"
                     /note="unknown protein"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="CAD38961.1"
                     /db_xref="GI:21739871"
                     /db_xref="UniProt/TrEMBL:Q8NDB7"
                     /translation="VLAAQPRRRPGTPVLCAKPWPRGPGHGPGARGEAASRGAVTGRA
                     SAMKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSV
                     TWLNRSKVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVFDW
                     NTPKKGGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFC
                     NFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGS
                     GNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQV
                     IFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPK
                     LEHPTQQDIDLYHTMYMEALVKLFDKHKTKFGLPETEVLEVN"
     polyA_signal    2309. .2314
                     /gene="DKFZp667C1711"
     polyA_site      2331
                     /gene="DKFZp667C1711"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 9;  Length 2364;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        836 GCATTGCCACTCCCATTCTT 817


RESULT 21
AX281630/c
LOCUS       AX281630               2398 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 39 from Patent WO0177389.
ACCESSION   AX281630
VERSION     AX281630.1  GI:16608881
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
            Mikita,T. and Tai,J.
  TITLE     Genes expressed in foam cell differentiation
  JOURNAL   Patent: WO 0177389-A 39 18-OCT-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2398
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 474682.2"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2398;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        903 GCATTGCCACTCCCATTCTT 884


RESULT 22
AX430071/c
LOCUS       AX430071               2418 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 5 from Patent WO0208260.
ACCESSION   AX430071
VERSION     AX430071.1  GI:21541219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R.
  TITLE     Bstp-ecg1 protein and related reagents and methods of use thereof
  JOURNAL   Patent: WO 0208260-A 5 31-JAN-2002;
            STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2418
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Consensus sequence derived from IMAGE clones"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2418;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        898 GCATTGCCACTCCCATTCTT 879


RESULT 23
BD181466/c
LOCUS       BD181466               2439 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  A gene of which expression changes in psoriasis and a method for e
            xamination directed to said gene.
ACCESSION   BD181466
VERSION     BD181466.1  GI:30792384
KEYWORDS    JP 2002330770-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2439)
  AUTHORS   Imai,Y., Wakimoto,K., Yamada,E., Chiba,H. and Okubo,K.
  TITLE     A gene of which expression changes in psoriasis and a method for e
            xamination directed to said gene
  JOURNAL   Patent: JP 2002330770-A 14 19-NOV-2002;
            TANABE SEIYAKU CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002330770-A/14
            PD   19-NOV-2002
            PF   25-MAY-2001 JP 2001156529
            PI   YUJI IMAI,KOJI WAKIMOTO,ERIKO YAMADA,HIROAKI CHIBA,KOSAKU  PI
             OKUBO
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC   A gene
            of which expression changes in psoriasis and a method  CC
             for e
            CC   xamination directed to said gene
            FH   Key             Location/Qualifiers
            FT   CDS             (231). .(1394).
FEATURES             Location/Qualifiers
     source          1. .2439
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2439;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        928 GCATTGCCACTCCCATTCTT 909


RESULT 24
AB048286/c
LOCUS       AB048286                2439 bp    mRNA    linear   PRI 09-OCT-2003
DEFINITION  Homo sapiens GS1999full mRNA, complete cds.
ACCESSION   AB048286
VERSION     AB048286.2  GI:22506630
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wakimoto,K., Chiba,H., Michibata,H., Seishima,M., Kawasaki,S.,
            Okubo,K., Mitsui,H., Torii,H. and Imai,Y.
  TITLE     A novel diacylglycerol acyltransferase (DGAT2) is decreased in
            human psoriatic skin and increased in diabetic mice
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2439)
  AUTHORS   Imai,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2000) Yuji Imai, Tanabe seiyaku Co.,Ltd.,
            Discovery Research Laboratory; Kashima 3-16-89, Yodogawa-ku, Osaka
            532-8505, Japan (E-mail:y-imai@tanabe.co.jp, Tel:81-6-6300-2931,
            Fax:81-6-6300-2590)
COMMENT     On Aug 26, 2002 this sequence version replaced gi:13537296.
FEATURES             Location/Qualifiers
     source          1. .2439
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_lib="spleen cDNA library"
     gene            1. .2439
                     /gene="GS1999full"
     CDS             231. .1397
                     /gene="GS1999full"
                     /note="product is unknown"
                     /codon_start=1
                     /protein_id="BAB40641.2"
                     /db_xref="GI:22506631"
                     /translation="MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGS
                     SILSALQDLFSVTWLNRSKVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI
                     AVLYFTWLVFDWNTPKKGGRRSQWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGY
                     HPHGIMGLGAFCNFSTEATEVSKKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVSR
                     DTIDYLLSKNGSGNAIIIVVGGAAESLSSMPGKNAVTLRNRKGFVKLALRHGADLVPI
                     YSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFHGRGLFSSDTWGLVPYSKPI
                     TTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFGLPETEVLEVN"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 9;  Length 2439;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        928 GCATTGCCACTCCCATTCTT 909


RESULT 25
AX430069/c
LOCUS       AX430069                2445 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 3 from Patent WO0208260.
ACCESSION   AX430069
VERSION     AX430069.1  GI:21541217
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Botstein,D., Brown,P.O., Perou,C., Ross,D. and Seitz,R.
  TITLE     Bstp-ecg1 protein and related reagents and methods of use thereof
  JOURNAL   Patent: WO 0208260-A 3 31-JAN-2002;
            STANFORD UNIVERSITY (US) ; Applied Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2445
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleotide sequence of a cDNA that encodes
                     BSTP-ECG1"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2445;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        925 GCATTGCCACTCCCATTCTT 906


RESULT 26
AX747231/c
LOCUS       AX747231                2678 bp    mRNA    linear   PAT 20-JUN-2003
DEFINITION  Sequence 756 from Patent EP1308459.
ACCESSION   AX747231
VERSION     AX747231.1  GI:32131619
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1308459-A 756 07-MAY-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .2678
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 2678;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       2085 GCATTGCCACTCCCATTCTT 2066


RESULT 27
AK091870/c
LOCUS       AK091870                2678 bp    mRNA    linear   PRI 30-JAN-2004
DEFINITION  Homo sapiens cDNA FLJ34551 fis, clone HLUNG2009413.
ACCESSION   AK091870
VERSION     AK091870.1  GI:21750339
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED 14702039
REFERENCE 2
AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2678)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
FEATURES Location/Qualifiers
source 1. .2678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HLUNG2009413"
/tissue_type="lung"
/clone_lib="HLUNG2"
/note="cloning vector: pME18SFL3"
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2678;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 2085 GCATTGCCACTCCCATTCTT 2066

RESULT 28
BD181467/c
LOCUS BD181467 2713 bp DNA linear PAT 15-MAY-2003
DEFINITION A gene of which expression changes in psoriasis and a method for examination directed to said gene.
ACCESSION BD181467
VERSION BD181467.1 GI:30792385
KEYWORDS JP 2002330770-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2713)
AUTHORS Imai,Y., Wakimoto,K., Yamada,E., Chiba,H. and Okubo,K.
TITLE A gene of which expression changes in psoriasis and a method for examination directed to said gene
JOURNAL Patent: JP 2002330770-A 15 19-NOV-2002;
TANABE SEIYAKU CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2002330770-A/15
PD 19-NOV-2002
PF 25-MAY-2001 JP 2001156529
PI YUJI IMAI,KOJI WAKIMOTO,ERIKO YAMADA,HIROAKI CHIBA,KOSAKU OKUBO PI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC ,C12N5/10,C12Q1/68,
PC G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC A gene of which expression changes in psoriasis and a method CC for e
CC xamination directed to said gene
FH Key Location/Qualifiers
FT CDS (778). .(1668).
FEATURES Location/Qualifiers
source 1. .2713
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2713;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 1202 GCATTGCCACTCCCATTCTT 1183

RESULT 29
BTA534371/c
LOCUS BTA534371 2788 bp DNA linear MAM 06-FEB-2004
DEFINITION Bos taurus DGAT2 gene for diacylglycerol O-acyltransferase 2, exons 5 to 7.
ACCESSION AJ534371
VERSION AJ534371.1 GI:42454650
KEYWORDS DGAT2 gene; diacylglycerol O-acyltransferase 2.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1
AUTHORS Winter,A., can Eckveld,M., Bininda Emonds,O.R.P., Habermann,F.A. and Fries,R.
TITLE Genomic organization of the dgat2/mogat gene family in cattle (bos

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            taurus) and other mammals
  JOURNAL   (er) Cytogenet. Genome Res. 102: DOI, 10.1159/000075723 (2003)
REFERENCE   2  (bases 1 to 2788)
  AUTHORS   Winter,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2002) Lehrstuhl fuer Tierzucht, Technischen
            Universitaet Muenchen, Alte Akademie 12, Freising-Weihenstephan
            85354, GERMANY
FEATURES             Location/Qualifiers
     source          1. .2788
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
     gene            1. .2788
                     /gene="DGAT2"
     intron          <1. .446
                     /gene="DGAT2"
                     /number=4
     exon            447. .651
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                     /number=5
                     /usedin=AJ534368:dgat2_cds
     intron          652. .1220
                     /gene="DGAT2"
                     /number=5
     exon            1221. .1395
                     /gene="DGAT2"
                     /number=6
                     /usedin=AJ534368:dgat2_cds
     intron          1396. .2197
                     /gene="DGAT2"
                     /number=6
     exon            2198. .2400
                     /gene="DGAT2"
                     /number=7
                     /usedin=AJ534368:dgat2_cds
     intron          2401. .>2788
                     /gene="DGAT2"
                     /number=7
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 2788;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       1284 GCATTGCCACTCCCATTCTT 1265


RESULT 30
AP003031/c
LOCUS       AP003031               95585 bp    DNA     linear   PRI 15-MAR-2003
DEFINITION  Homo sapiens genomic DNA, chromosome 11q clone:RP11-535A19,
            complete sequences.
ACCESSION   AP003031
VERSION     AP003031.3  GI:17939953
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 95585)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-2000) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On Dec 19, 2001 this sequence version replaced gi:14625395.
FEATURES             Location/Qualifiers
     source          1. .95585
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q"
                     /clone="RP11-535A19"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 95585;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       7993 GCATTGCCACTCCCATTCTT 7974


RESULT 31
AC111120/c
LOCUS       AC111120               146346 bp    DNA     linear   HTG 18-SEP-2004
DEFINITION  Mus musculus chromosome 7 clone RP23-225M4 map 7, *** SEQUENCING IN
            PROGRESS ***, 8 unordered pieces.
ACCESSION   AC111120
VERSION     AC111120.4  GI:52319138
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 146346)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 7, clone RP23-225M4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 146346)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C.,
            Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
            McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman;C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
            Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
            Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 146346)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
            Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
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            Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Sep 18, 2004 this sequence version replaced gi:45917434.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
            -------------- Project Information
                Center project name: L22508
                Center clone name: 225_M_4
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     7912: contig of 7912 bp in length
            *     7913     8012: gap of unknown length
            *     8013    36022: contig of 28010 bp in length
            *    36023    36122: gap of unknown length
            *    36123    49863: contig of 13741 bp in length
            *    49864    49963: gap of unknown length
            *    49964    56757: contig of 6794 bp in length
            *    56758    56857: gap of unknown length
            *    56858    59875: contig of 3018 bp in length
            *    59876    59975: gap of unknown length
            *    59976    80009: contig of 20034 bp in length
            *    80010    80109: gap of unknown length
            *    80110    88875: contig of 8766 bp in length
            *    88876    88975: gap of unknown length
            *    88976   146346: contig of 57371 bp in length.
FEATURES            Location/Qualifiers
     source         1. .146346
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:10090"
                    /chromosome="7"
                    /map="7"
                    /clone="RP23-225M4"
                    /clone_lib="RPCI-23 Female Mouse BAC"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 146346;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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Db     130951 GCATTGCCACTCCCATTCTT 130932
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RESULT 32
AC115850/c
LOCUS       AC115850              155227 bp    DNA     linear   HTG 13-OCT-2004
DEFINITION  Mus musculus chromosome 7 clone RP24-252O10 map 7, *** SEQUENCING
            IN PROGRESS ***, 4 unordered pieces.
ACCESSION   AC115850
VERSION     AC115850.7  GI:54111344
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 155227)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 7, clone RP24-252O10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155227)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
            Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 155227)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
            Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 13, 2004 this sequence version replaced gi:51889862.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
```

```
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@broad.mit.edu
          ---------- Project Information
            Center project name: L24674
            Center clone name: 252_O_10
          ----------.
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 4 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *        1    45393: contig of 45393 bp in length
          *    45394    45493: gap of unknown length
          *    45494    94478: contig of 48985 bp in length
          *    94479    94578: gap of unknown length
          *    94579   113577: contig of 18999 bp in length
          *   113578   113677: gap of unknown length
          *   113678   155227: contig of 41550 bp in length.
FEATURES             Location/Qualifiers
     source          1. .155227
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="7"
                     /map="7"
                     /clone="RP24-252O10"
                     /clone_lib="RPCI-24 Male Mouse BAC"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 155227;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db      37818 GCATTGCCACTCCCATTCTT 37799


RESULT 33
AC021221
LOCUS       AC021221              162719 bp    DNA     linear   HTG 07-JUL-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-535A19, WORKING DRAFT
            SEQUENCE, 16 unordered pieces.
ACCESSION   AC021221
VERSION     AC021221.3  GI:7232190
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 162719)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 162719)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Mar 13, 2000 this sequence version replaced gi:7024104.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0535A19
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 91%
            Sequencing vector: plasmid; 9%
            Chemistry: Dye-primer ET; 91% of reads
            Chemistry: Dye-terminator Big Dye; 9% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 151216 bases at least Q40
            Consensus quality: 155281 bases at least Q30
            Consensus quality: 157953 bases at least Q20
            Insert size: 168000; agarose-fp
            Insert size: 161219; sum-of-contigs
            Quality coverage: 3.91 in Q20 bases; agarose-fp
            Quality coverage: 4.11 in Q20 bases; sum-of-contigs
            ----------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 16 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1113: contig of 1113 bp in length
            *     1114     1213: gap of unknown length
            *     1214     3315: contig of 2102 bp in length
            *     3316     3415: gap of unknown length
            *     3416     5298: contig of 1883 bp in length
            *     5299     5398: gap of unknown length
            *     5399     8550: contig of 3152 bp in length
            *     8551     8650: gap of unknown length
            *     8651    12595: contig of 3945 bp in length
            *    12596    12695: gap of unknown length
            *    12696    17345: contig of 4650 bp in length
            *    17346    17445: gap of unknown length
            *    17446    21339: contig of 3894 bp in length
            *    21340    21439: gap of unknown length
            *    21440    26989: contig of 5550 bp in length
            *    26990    27089: gap of unknown length
            *    27090    34149: contig of 7060 bp in length
            *    34150    34249: gap of unknown length
            *    34250    47612: contig of 13363 bp in length
            *    47613    47712: gap of unknown length
            *    47713    59240: contig of 11528 bp in length
            *    59241    59340: gap of unknown length
            *    59341    74225: contig of 14885 bp in length
            *    74226    74325: gap of unknown length
            *    74326    89758: contig of 15433 bp in length
            *    89759    89858: gap of unknown length
            *    89859   108185: contig of 18327 bp in length
            *   108186   108285: gap of unknown length
            *   108286   132109: contig of 23824 bp in length
            *   132110   132209: gap of unknown length
            *   132210   162719: contig of 30510 bp in length.
FEATURES             Location/Qualifiers
     source          1. .162719
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /clone="RP11-535A19"
     misc_feature    1. .1113
                     /note="assembly_name:Contig3"
     misc_feature    1214. .3315
                     /note="assembly_name:Contig4"
     misc_feature    3416. .5298
                     /note="assembly_name:Contig5"
     misc_feature    5399. .8550
                     /note="assembly_name:Contig6"
     misc_feature    8651. .12595
                     /note="assembly_name:Contig7
                     clone_end:SP6
                     vector_side:left"
     misc_feature    12696. .17345
                     /note="assembly_name:Contig8"
```

```
     misc_feature    17446. .21339
                     /note="assembly_name:Contig9"
     misc_feature    21440. .26989
                     /note="assembly_name:Contig10"
     misc_feature    27090. .34149
                     /note="assembly_name:Contig11"
     misc_feature    34250. .47612
                     /note="assembly_name:Contig12"
     misc_feature    47713. .59240
                     /note="assembly_name:Contig13"
     misc_feature    59341. .74225
                     /note="assembly_name:Contig14"
     misc_feature    74326. .89758
                     /note="assembly_name:Contig15"
     misc_feature    89859. .108185
                     /note="assembly_name:Contig16"
     misc_feature    108286. .132109
                     /note="assembly_name:Contig17"
     misc_feature    132210. .162719
                     /note="assembly_name:Contig18"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 162719;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db     111632 GCATTGCCACTCCCATTCTT 111651


RESULT 34
AY589091S2/c
LOCUS       AY589091S2               721 bp    DNA     linear   MAM 04-MAY-2004
DEFINITION  Bos taurus diacylglycerol O-acyltransferase 2 (DGAT2) gene, exons
            5, 6 and partial cds.
ACCESSION   AY589092
VERSION     AY589092.1  GI:46850516
KEYWORDS    .
SEGMENT     2 of 4
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 721)
  AUTHORS   Xu,X.R., Xu,S.Z. and Li,J.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2004) Department of Animal Science, Academic of
            Agriculture Science of China, Haidian District, Beijing 100094,
            China
FEATURES             Location/Qualifiers
     source          1. .721
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
     mRNA            join(<1. .90,659. .>721)
                     /gene="DGAT2"
                     /product="diacylglycerol O-acyltransferase 2"
     CDS             join(<1. .90,659. .>721)
                     /gene="DGAT2"
                     /codon_start=3
                     /product="diacylglycerol O-acyltransferase 2"
                     /protein_id="AAT02658.1"
                     /db_xref="GI:46850520"
                     /translation="KKFPGIRPYLATLAGNFRMPVLREYLMSGGICPVNRDTIDYLLS
                     KNGSGN"
     exon            <1. .90
                     /gene="DGAT2"
                     /number=5
     exon            659. .>721
                     /gene="DGAT2"
                     /number=6
ORIGIN

  Query Match             95.0%;  Score 19;  DB 4;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 0.64;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        721 CATTGCCACTCCCATTCTT 703


RESULT 35
AE004034
LOCUS       AE004034                 10013 bp    DNA     linear   BCT 04-JUN-2004
DEFINITION  Xylella fastidiosa 9a5c, section 180 of 229 of the complete genome.
ACCESSION   AE004034 AE003849
VERSION     AE004034.1  GI:9107358
KEYWORDS    .
SOURCE      Xylella fastidiosa 9a5c
  ORGANISM  Xylella fastidiosa 9a5c
            Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
            Xanthomonadaceae; Xylella.
REFERENCE   1  (bases 1 to 10013)
  AUTHORS   Simpson,A.J., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
            Alvarenga,R., Alves,L.M., Araya,J.E., Baia,G.S., Baptista,C.S.,
            Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.,
            Bueno,M.R., Camargo,A.A., Camargo,L.E., Carraro,D.M., Carrer,H.,
            Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C., Costa-Neto,C.M.,
            Coutinho,L.L., Cristofani,M., Dias-Neto,E., Docena,C., El-Dorry,H.,
            Facincani,A.P., Ferreira,A.J., Ferreira,V.C., Ferro,J.A.,
            Fraga,J.S., Franca,S.C., Franco,M.C., Frohme,M., Furlan,L.R.,
            Garnier,M., Goldman,G.H., Goldman,M.H., Gomes,S.L., Gruber,A.,
            Ho,P.L., Hoheisel,J.D., Junqueira,M.L., Kemper,E.L., Kitajima,J.P.
            and Marino,C.L.
  TITLE     The genome sequence of the plant pathogen Xylella fastidiosa. The
            Xylella fastidiosa Consortium of the Organization for Nucleotide
            Sequencing and Analysis
  JOURNAL   Nature 406 (6792), 151-157 (2000)
  MEDLINE   20365717
   PUBMED   10910347
REFERENCE   2  (bases 1 to 10013)
  AUTHORS   Simpson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M.,
            Alvarenga,R., Alves,L.M.C., Araya,J.E., Baia,G.S., Baptista,C.S.,
            Barros,M.H., Bonaccorsi,E.D., Bordin,S., Bove,J.M., Briones,M.R.S.,
            Bueno,M.R.P., Camargo,A.A., Camargo,L.E.A., Carraro,D.M.,
            Carrer,H., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C.R.,
            Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E.,
            Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S.,
            Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Franco,M.C.,
            Frohme,M., Furlan,L.R., Garnier,M., Goldman,G.H., Goldman,M.H.S.,
            Gomes,S.L., Gruber,A., Ho,P.L., Hoheisel,J.D., Junqueira,M.L.,
            Kemper,E.L., Kitajima,J.P., Krieger,J.E., Kuramae,E.E., Laigret,F.,
            Lambais,M.R., Leite,L.C.C., Lemos,E.G.M., Lemos,M.V.F., Lopes,S.A.,
            Lopes,C.R., Machado,J.A., Machado,M.A., Madeira,A.M.B.N.,
            Madeira,H.M.F., Marino,C.L., Marques,M.V., Martins,E.A.L.,
            Martins,E.M.F., Matsukuma,A.Y., Menck,C.F.M., Miracca,E.C.,
            Miyaki,C.Y., Monteiro-Vitorello,C.B., Moon,D.H., Nagai,M.A.,
            Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.,A., Nobrega,F.G.,
            Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C.,
            Palmieri,D.A., Paris,A., Peixoto,B.R., Pereira,G.A.G., Pereira
            Jr.,H.A., Pesquero,J.B., Quaggio,R.B., Roberto,P.G., Rodrigues,V.,
            de M. Rosa,A.J., de Rosa Jr.,V.E., de Sa,R.G., Santelli,R.V.,
            Sawasaki,H.E., da Silva,A.C.R., da Silva,F.R., da Silva,A.M., Silva
            Jr.,W.A., da Silveira,J.F., Silvestri,M.L.Z., Siqueira,W.J., de
            Souza,A.A., de Souza,A.P., Terenzi,M.F., Truffi,D., Tsai,S.M.,
            Tsuhako,M.H., Vallada,H., Van Sluys,M.A., Verjovski-Almeida,S.,
            Vettore,A.L., Zago,M.A., Zatz,M., Meidanis,J. and Setubal,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and
            Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
            13083-970, Brazil
FEATURES             Location/Qualifiers
     source          1. .10013
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/organism="Xylella fastidiosa 9a5c"
/mol_type="genomic DNA"
/db_xref="taxon:160492"
/clone="9a5c"

gene 70. .237
/locus_tag="XF2212"

CDS 70. .237
/locus_tag="XF2212"
/note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAF85011.1"
/db_xref="GI:9107359"
/translation="MHPDNALKKQPHLEALHQSSATALLVLINLSRRNSATATLRAAG
NTPSALTMPCL"

gene complement(217. .837)
/locus_tag="XF2213"

CDS complement(217. .837)
/locus_tag="XF2213"
/note="similar to SP|O24714 (percent identity: 56 %/query alignment coverage: 93.7 %/subject alignment coverage: 97.5 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase bifunctional enzyme"
/protein_id="AAF85012.1"
/db_xref="GI:9107360"
/translation="MCNEPATSDVALPDLDWAKGDGLLPVIVQDADTLRVLMLGYMNS
QALEVTQRSRLVTFYSRSKQRLWTKGERSGHVLHLVAIDADCDADTLLVQARPRGPTC
HLGRTSCFPAAPGQFLGALDALVAERERERPQDSYTTALFEQGVRRIAQKVGEEGVET
ALAGVVQVDDALLDESADLLYHLIVLLRARGLSLADAVTVLEARHR"

gene complement(830. .1603)
/locus_tag="XF2214"

CDS complement(830. .1603)
/locus_tag="XF2214"
/note="similar to SP|P45603 (percent identity: 61 %/query alignment coverage: 99.6 %/subject alignment coverage: 99.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="cyclase"
/protein_id="AAF85013.1"
/db_xref="GI:9107361"
/translation="MLSRRLIPCLDVRDGRVVKGVKFRDHVDMGDIVELALRYRDHGA
DELVFYDIGASPRGRSVDYRWVERVARLIDIPFCVAGGIGQVETARAVLHAGADKISI
NSPALRQPALISALAEAFGVQCVVVGIDSIREADGQWRVRCNTGDPDKTQALPLRTLD
WIVEAQRLGAGEIVLNCMDSDGVRCGYDIAQLSQARALCQVPLVASGGAGNMQHFADV
FHKADVDGALAASVFHSGAILIPGLKQFLREQQIEVRDV"

gene complement(1728. .2525)
/locus_tag="XF2215"

CDS complement(1728. .2525)
/locus_tag="XF2215"
/note="similar to SP|P10371 (percent identity: 44 %/query alignment coverage: 90.2 %/subject alignment coverage: 97.6 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase"
/protein_id="AAF85014.1"
/db_xref="GI:9107362"
/translation="MNFIVYPALDIRNGAVVRLQQGDYARQTRYDDQVLPRALAFADS
GATWMHLVDLDAAKAGGYTLAPLLRQMTRATGLQVQTGGGVRSRDDVARILDAGAARV
VIGSLAVRESARVIEWLQAFGPERITVALDTRQDAGGVWRLPVHGWTEVAEATLDVLA
QQYAAAGLRHLLCTDIARDGMLSGPNMDVYTYLRALVPAVQLQVSGGARDVADVVAAK
MAGCAGIVLGKALLEGRLALKEAVQQGSVADPSDPLPCGELTEPVCR"

gene complement(2522. .3124)
/locus_tag="XF2216"

CDS complement(2522. .3124)
/locus_tag="XF2216"
/note="similar to SP|P44340 (percent identity: 43 %/query alignment coverage: 98.0 %/subject alignment coverage: 98.5 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="amidotransferase"
/protein_id="AAF85015.1"
/db_xref="GI:9107363"
/translation="MTEVALIDAGGANLGSVRYALQRLGVEPRLVCDARGLEGAARVI
LPGVGSAPEAMARLNNQGLIEPLLRLQVPLIGICLGMQLLFEHSEEGDVPCLALLPGR
VRRLTPAPSIRVPHMGWNRLLPLRASPLLAEVPEGASAYFVHSYAVPLTTAAVAACDH
GGMFTAIVQQGVRCGAQFHPERSAETGARILRNFLEMDAA"

gene complement(3121. .4248)
/locus_tag="XF2217"

CDS complement(3121. .4248)
/locus_tag="XF2217"
/note="similar to SP|P06987 (percent identity: 50 %/query alignment coverage: 99.2 %/subject alignment coverage: 104.8 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="imidazoleglycerolphosphate dehydratase/histidinol-phosphate phosphatase bifunctional enzyme"
/protein_id="AAF85016.1"
/db_xref="GI:9107364"
/translation="MTPIVFIDRDGTLIEEPPDFQIDAYEKLRLVNGVIPALLKLRDA
GYHFVIVTNQDGLGSPAYPQASFDGPNALMLQIFSSQGIVFRDVLIDRSWPTDNAPTR
KPGIGLMVAYLQDRDIDWARSAMVGDRPTDLQFAENLNIRGFQLRTPQFGGDWDWDGI
AHTLADAPRRAVVQRHTKETTIRVEIDLDGAPQARITTGLPFFDHMLEQIAKHAGISL
QISAVGDLHIDEHHTIEDTGLALGQAVRQALGDKRGIGRYGFDPPQLPWQVSGAAAHG
GFTLPMDETQASAVLDFSGRPYCVFEGTFVRERVGDMPTELVPHFFRSLCDASGMNLH
LSVHGDNDHHKVEACFKALARALRQALQRHGHVLPSTKGAL"

gene complement(4245. .5342)
/locus_tag="XF2218"

CDS complement(4245. .5342)
/locus_tag="XF2218"
/note="similar to SP|P06986 (percent identity: 42 %/query alignment coverage: 97.8 %/subject alignment coverage: 100.3 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
/transl_table=11
/product="histidinol-phosphate aminotransferase"
/protein_id="AAF85017.1"
/db_xref="GI:9107365"
/translation="MNTQTPTVLDLVRQELRNFAGYSSARSVALTGDLWLNANESAWP
NPADSHATMRRYPEPQPPKLRQMLAALYGCVPEQLLIGRGSDEGIDLLVRAVCEPGCD
PVLVTPPVFGMYAVSAQLQNAPVIQVPLVDDAAGFHADVPAIITAAQTSRAKLVFLCS
PSNPVGAAIPLQQIETILQTLAGTALVVVDEAYGEFSDVPSVVPLLARYPHLVVLRTL
SKAHALAAVRIGSVIADAHLVAILRRCQAPYPLPTPCVSLAEQGLSAAALQVTAQRVA
EIRAERERLGAALACLSGVRRVYPSQGNFLLVRFDDAEAALQALYAAGVVVRDQRAAP
QLHDALRLTVGTPEQNTRLLAVLRDIQAVPA"

gene complement(5339. .6634)
/locus_tag="XF2219"

CDS complement(5339. .6634)
/locus_tag="XF2219"
/note="similar to SP|P06988 (percent identity: 50 %/query alignment coverage: 99.5 %/subject alignment coverage: 98.8 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"

Query Match 85.0%; Score 17; DB 1; Length 10013;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGCCACTCCCATTCTT 20

```
                ||||||||||||||||
Db       7177 TTGCCACTCCCATTCTT 7193


RESULT 36
AL954659/c
LOCUS       AL954659               43593 bp    DNA     linear   PRI 02-DEC-2002
DEFINITION  Human DNA sequence from clone RP11-142D11 on chromosome X, complete
            sequence.
ACCESSION   AL954659
VERSION     AL954659.4  GI:26185670
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43593)
  AUTHORS   Wray,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Dec 6, 2002 this sequence version replaced gi:25809658.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome X, constructed by the Sanger Centre Chromosome X Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX
            RP11-142D11 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .43593
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /clone="RP11-142D11"
                     /clone_lib="RPCI-11.1"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 43593;
  Best Local Similarity   100.0%;  Pred. No. 7.8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db      29329 CATTGCCACTCCCATTC 29313


RESULT 37
AC100360
LOCUS       AC100360               69294 bp    DNA     linear   HTG 22-NOV-2001
DEFINITION  Mus musculus clone RP23-128F24, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC100360
VERSION     AC100360.1  GI:17047726
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 69294)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP23-128F24
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 69294)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L15164
                Center clone name: 128_F_24
            --------------.
            * NOTE: This record contains 67 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      946: contig of 946 bp in length
            *      947     1046: gap of 100 bp
            *     1047     2020: contig of 974 bp in length
            *     2021     2120: gap of 100 bp
            *     2121     3095: contig of 975 bp in length
            *     3096     3195: gap of 100 bp
            *     3196     4186: contig of 991 bp in length
```

```
*     4187     4286: gap of 100 bp
*     4287     5159: contig of 873 bp in length
*     5160     5259: gap of 100 bp
*     5260     6149: contig of 890 bp in length
*     6150     6249: gap of 100 bp
*     6250     7179: contig of 930 bp in length
*     7180     7279: gap of 100 bp
*     7280     8280: contig of 1001 bp in length
*     8281     8380: gap of 100 bp
*     8381     9379: contig of 999 bp in length
*     9380     9479: gap of 100 bp
*     9480    10468: contig of 989 bp in length
*    10469    10568: gap of 100 bp
*    10569    11550: contig of 982 bp in length
*    11551    11650: gap of 100 bp
*    11651    12588: contig of 938 bp in length
*    12589    12688: gap of 100 bp
*    12689    13630: contig of 942 bp in length
*    13631    13730: gap of 100 bp
*    13731    14568: contig of 838 bp in length
*    14569    14668: gap of 100 bp
*    14669    15636: contig of 968 bp in length
*    15637    15736: gap of 100 bp
*    15737    16706: contig of 970 bp in length
*    16707    16806: gap of 100 bp
*    16807    17719: contig of 913 bp in length
*    17720    17819: gap of 100 bp
*    17820    18737: contig of 918 bp in length
*    18738    18837: gap of 100 bp
*    18838    19769: contig of 932 bp in length
*    19770    19869: gap of 100 bp
*    19870    20863: contig of 994 bp in length
*    20864    20963: gap of 100 bp
*    20964    21918: contig of 955 bp in length
*    21919    22018: gap of 100 bp
*    22019    22958: contig of 940 bp in length
*    22959    23058: gap of 100 bp
*    23059    23918: contig of 860 bp in length
*    23919    24018: gap of 100 bp
*    24019    24974: contig of 956 bp in length
*    24975    25074: gap of 100 bp
*    25075    26101: contig of 1027 bp in length
*    26102    26201: gap of 100 bp
*    26202    26944: contig of 743 bp in length
*    26945    27044: gap of 100 bp
*    27045    27779: contig of 735 bp in length
*    27780    27879: gap of 100 bp
*    27880    28860: contig of 981 bp in length
*    28861    28960: gap of 100 bp
*    28961    29882: contig of 922 bp in length
*    29883    29982: gap of 100 bp
*    29983    30957: contig of 975 bp in length
*    30958    31057: gap of 100 bp
*    31058    32006: contig of 949 bp in length
*    32007    32106: gap of 100 bp
*    32107    33030: contig of 924 bp in length
*    33031    33130: gap of 100 bp
*    33131    34113: contig of 983 bp in length
*    34114    34213: gap of 100 bp
*    34214    35121: contig of 908 bp in length
*    35122    35221: gap of 100 bp
*    35222    36181: contig of 960 bp in length
*    36182    36281: gap of 100 bp
*    36282    36968: contig of 687 bp in length
*    36969    37068: gap of 100 bp
*    37069    37989: contig of 921 bp in length
*    37990    38089: gap of 100 bp
*    38090    38998: contig of 909 bp in length
*    38999    39098: gap of 100 bp
*    39099    40029: contig of 931 bp in length
*    40030    40129: gap of 100 bp
*    40130    41007: contig of 878 bp in length
*    41008    41107: gap of 100 bp
*    41108    42090: contig of 983 bp in length
*    42091    42190: gap of 100 bp
*    42191    43100: contig of 910 bp in length
*    43101    43200: gap of 100 bp
*    43201    44181: contig of 981 bp in length
*    44182    44281: gap of 100 bp
*    44282    45318: contig of 1037 bp in length
*    45319    45418: gap of 100 bp
*    45419    46357: contig of 939 bp in length
*    46358    46457: gap of 100 bp
*    46458    47408: contig of 951 bp in length
*    47409    47508: gap of 100 bp
*    47509    48412: contig of 904 bp in length
*    48413    48512: gap of 100 bp
*    48513    49448: contig of 936 bp in length
*    49449    49548: gap of 100 bp
*    49549    50533: contig of 985 bp in length
*    50534    50633: gap of 100 bp
*    50634    51583: contig of 950 bp in length
*    51584    51683: gap of 100 bp
*    51684    52692: contig of 1009 bp in length
*    52693    52792: gap of 100 bp
*    52793    53730: contig of 938 bp in length
*    53731    53830: gap of 100 bp
*    53831    54735: contig of 905 bp in length
*    54736    54835: gap of 100 bp
*    54836    55763: contig of 928 bp in length
*    55764    55863: gap of 100 bp
*    55864    56842: contig of 979 bp in length
*    56843    56942: gap of 100 bp
*    56943    57873: contig of 931 bp in length
*    57874    57973: gap of 100 bp
*    57974    58882: contig of 909 bp in length
*    58883    58982: gap of 100 bp
*    58983    59996: contig of 1014 bp in length
*    59997    60096: gap of 100 bp
*    60097    61082: contig of 986 bp in length
*    61083    61182: gap of 100 bp
*    61183    62100: contig of 918 bp in length
*    62101    62200: gap of 100 bp
*    62201    62916: contig of 716 bp in length
*    62917    63016: gap of 100 bp
*    63017    63950: contig of 934 bp in length
*    63951    64050: gap of 100 bp
*    64051    64958: contig of 908 bp in length
*    64959    65058: gap of 100 bp
*    65059    66060: contig of 1002 bp in length
*    66061    66160: gap of 100 bp
*    66161    67113: contig of 953 bp in length
*    67114    67213: gap of 100 bp
*    67214    68204: contig of 991 bp in length
*    68205    68304: gap of 100 bp
*    68305    69294: contig of 990 bp in length.
FEATURES             Location/Qualifiers
     source          1. .69294
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"

  Query Match             85.0%;  Score 17;  DB 2;  Length 69294;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATT 17
              |||||||||||||||||
Db      37682 GCATTGCCACTCCCATT 37698


RESULT 38
AL365359/c
LOCUS       AL365359               98637 bp    DNA     linear   HTG 10-JUL-2001
DEFINITION  Homo sapiens chromosome 1 clone RP5-1028I1, 7 unordered pieces.
ACCESSION   AL365359
```

```
VERSION     AL365359.7  GI:11322090
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mclay,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 23, 2000 this sequence version replaced gi:9926733.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: dJ1028I1
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry:
            Dye-terminator Big Dye; 83% of reads
            Consensus quality: 95773 bases at least Q40
            Consensus quality: 96880 bases at least Q30
            Consensus quality: 97481 bases at least Q20
            Insert size: 98037; sum-of-contigs
            Insert size: 94436; 8.5% error; agarose-fp
            Quality coverage: 6.23x in Q20 bases; sum-of-contigs Quality
            coverage: 8.33x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     6481: contig of 6481 bp in length
            *     6482     6581: gap of 100 bp
            *     6582     9621: contig of 3040 bp in length
            *     9622     9721: gap of 100 bp
            *     9722    12293: contig of 2572 bp in length
            *    12294    12393: gap of 100 bp
            *    12394    47167: contig of 34774 bp in length
            *    47168    47267: gap of 100 bp
            *    47268    51868: contig of 4601 bp in length
            *    51869    51968: gap of 100 bp
            *    51969    66325: contig of 14357 bp in length
            *    66326    66425: gap of 100 bp
            *    66426    98637: contig of 32212 bp in length.
FEATURES             Location/Qualifiers
     source          1. .98637
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /clone="RP5-1028I1"
                     /clone_lib="RPCI-5"
     misc_feature    1. .6481
                     /note="assembly_fragment:01304
                     clone_end:SP6
                     vector_side:left"
     misc_feature    6582. .9621
                     /note="assembly_fragment:01036"
     misc_feature    9722. .12293
                     /note="assembly_fragment:01668"
     misc_feature    12394. .47167
                     /note="assembly_fragment:01209
                     fragment_chain:1"
     misc_feature    47268. .51868
                     /note="assembly_fragment:01171
                     fragment_chain:1"
     misc_feature    51969. .66325
                     /note="assembly_fragment:00109
                     fragment_chain:1"
     misc_feature    66426. .98637
                     /note="assembly_fragment:00843
                     fragment_chain:1
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 98637;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db      17355 CATTGCCACTCCCATTC 17339


RESULT 39
HSDJ96108
LOCUS       HSDJ96108             104695 bp    DNA     linear   PRI 17-APR-2001
DEFINITION  Human DNA sequence from clone RP5-96108 on chromosome X Contains
            STSs and GSSs, complete sequence.
ACCESSION   AL121879
VERSION     AL121879.14  GI:6635883
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 104695)
  AUTHORS   Bird,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Dec 26, 1999 this sequence version replaced gi:6630795.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
            the entire insert of clone RP5-96108 This sequence was generated
            from part of bacterial clone contigs of human chromosome X,
            constructed by the Sanger Centre Chromosome X Mapping Group.
            Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. RP5-96108 is from the
            library RPCI-5 constructed by the group of Pieter de Jong. For
            further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2.
FEATURES             Location/Qualifiers
     source          1. .104695
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
```

```
                /chromosome="X"
                /clone="RP5-96108"
                /clone_lib="RPCI-5"
repeat_region   1. .272
                /note="Charlie3 repeat: matches 1. .272 of consensus"
repeat_region   304. .903
                /note="LTR12 repeat: matches 1. .541 of consensus"
repeat_region   924. .3841
                /note="HERV9 repeat: matches 58. .2972 of consensus"
repeat_region   3841. .7462
                /note="HERV9 repeat: matches 4756. .8399 of consensus"
repeat_region   7492. .8427
                /note="LTR12 repeat: matches 323. .2438 of consensus"
misc_feature    complement(8445. .8612)
                /note="match: STS: Em:L15215"
repeat_region   9370. .9485
                /note="L2 repeat: matches 2629. .2748 of consensus"
repeat_region   9505. .9560
                /note="MIR repeat: matches 70. .129 of consensus"
repeat_region   9628. .11133
                /note="L1P repeat: matches 1. .1508 of consensus"
repeat_region   11132. .14428
                /note="L1PA4 repeat: matches 2812. .6142 of consensus"
repeat_region   14439. .14652
                /note="MIR repeat: matches 20. .213 of consensus"
repeat_region   15555. .15616
                /note="L2 repeat: matches 2264. .2311 of consensus"
repeat_region   15617. .15915
                /note="AluY repeat: matches 5. .302 of consensus"
repeat_region   15916. .15985
                /note="L2 repeat: matches 2190. .2264 of consensus"
misc_feature    16270. .16714
                /note="match: STS: Em:HSC76C4"
repeat_region   16600. .16867
                /note="L1MB2 repeat: matches 5888. .6155 of consensus"
repeat_region   17004. .17145
                /note="L2 repeat: matches 2553. .2701 of consensus"
repeat_region   18344. .18576
                /note="MIR repeat: matches 20. .252 of consensus"
repeat_region   19188. .19654
                /note="L1PB3 repeat: matches 5689. .6148 of consensus"
repeat_region   19655. .19748
                /note="L1MA2 repeat: matches 6213. .6308 of consensus"
repeat_region   19749. .19825
                /note="L1PB3 repeat: matches 5612. .5689 of consensus"
repeat_region   20297. .20727
                /note="L1ME3 repeat: matches 5157. .5580 of consensus"
repeat_region   20728. .21249
                /note="L1MB3 repeat: matches 5648. .6178 of consensus"
repeat_region   21250. .21803
                /note="L1ME3 repeat: matches 5580. .6163 of consensus"
misc_feature    complement(23018. .23146)
                /note="match: STS: Em:L41074"
repeat_region   23979. .24205
                /note="MIR repeat: matches 15. .235 of consensus"
repeat_region   25470. .25699
                /note="MER46A repeat: matches 2. .236 of consensus"
repeat_region   25769. .26063
                /note="L2 repeat: matches 2367. .2669 of consensus"
repeat_region   26092. .26573
                /note="L2 repeat: matches 916. .1407 of consensus"
repeat_region   26574. .27190
                /note="L1PA5 repeat: matches 5524. .6141 of consensus"
repeat_region   27191. .27420
                /note="L2 repeat: matches 1407. .1634 of consensus"
repeat_region   27863. .27961
                /note="L1MA6 repeat: matches 6202. .6300 of consensus"
repeat_region   28341. .28439
                /note="MIR repeat: matches 97. .202 of consensus"
repeat_region   28880. .28937
                /note="29 copies 2 mer ta 72% conserved"
repeat_region   29100. .29360
                /note="L2 repeat: matches 2406. .2648 of consensus"
repeat_region   29912. .30599
                /note="L2 repeat: matches 2003. .2710 of consensus"
misc_feature    31474. .31981
                /note="match: GSS: Em:AQ411673"
misc_feature    31501. .31774
                /note="match: GSS: Em:AQ570877"
repeat_region   31941. .32122
                /note="MIR repeat: matches 23. .205 of consensus"
repeat_region   32136. .32165
                /note="L1MA9 repeat: matches 6274. .6303 of consensus"
repeat_region   32769. .32949
                /note="MIR repeat: matches 20. .203 of consensus"
repeat_region   36212. .36427
                /note="MIR repeat: matches 2. .231 of consensus"
repeat_region   36925. .37076
                /note="Charlie4 repeat: matches 1801. .1955 of consensus"
repeat_region   37146. .37333
                /note="Charlie4 repeat: matches 1. .216 of consensus"
repeat_region   37724. .38038
                /note="AluSg repeat: matches 1. .310 of consensus"
repeat_region   38225. .38346
                /note="L2 repeat: matches 2371. .2491 of consensus"
repeat_region   39416. .39653
                /note="MIR repeat: matches 2. .241 of consensus"
repeat_region   40301. .40477
                /note="L1MA3 repeat: matches 6100. .6275 of consensus"
repeat_region   40503. .40542
                /note="20 copies 2 mer ta 90% conserved"
repeat_region   40543. .40872
                /note="165 copies 2 mer at 76% conserved"
repeat_region   40893. .41008
                /note="58 copies 2 mer ta 82% conserved"
misc_feature    40994
                /note="Tandem repeat. Forced join. gap sized to be less
                than 100 bases from restriction digest data and a spanning
                pUC clone."
repeat_region   41535. .42210
                /note="L1ME2 repeat: matches 5502. .6164 of consensus"
misc_feature    complement(42043. .42740)
                /note="match: GSS: Em:AQ488567"
repeat_region   42258. .42546
                /note="LTR39 repeat: matches 410. .960 of consensus"
misc_feature    complement(42377. .42743)
                /note="match: GSS: Em:AQ169848"
repeat_region   42593. .42850
                /note="MER49 repeat: matches 1. .294 of consensus"
misc_feature    42763. .43219
                /note="match: GSS: Em:AQ013777"
repeat_region   42900. .42993
                /note="LTR29 repeat: matches 3. .99 of consensus"
repeat_region   43421. .43472
                /note="MER39b repeat: matches 496. .547 of consensus"
repeat_region   43554. .43822
                /note="L1ME2 repeat: matches 5219. .5481 of consensus"
repeat_region   43875. .44159
                /note="L1PA8 repeat: matches 5589. .5874 of consensus"
repeat_region   44198. .45601
                /note="L1M4 repeat: matches 246. .1697 of consensus"
repeat_region   45911. .46342
                /note="MER41C repeat: matches 1. .508 of consensus"
repeat_region   46343. .46406
                /note="MER41-internal repeat: matches 80. .142 of
                consensus"
misc_feature    46423. .46757
                /note="match: GSS: Em:AQ099828"
repeat_region   46664. .47242
                /note="HERVE repeat: matches 3388. .3967 of consensus"
misc_feature    complement(47170. .47402)
                /note="match: GSS: Em:AQ041904"
repeat_region   47473. .48633
                /note="HERV9 repeat: matches 4694. .5853 of consensus"
misc_feature    48403. .48866
                /note="match: GSS: Em:AQ143235"
```

```
     misc_feature    48403. .48862
                     /note="match: GSS: Em:AQ544261"
     misc_feature    48403. .48838
                     /note="match: GSS: Em:AQ144565"
     misc_feature    48403. .48817

  Query Match             85.0%;  Score 17;  DB 9;  Length 104695;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db       5824 CATTGCCACTCCCATTC 5840


RESULT 40
AC130947_2
WPCOMMENT
  Sequence split into 5 fragments  LOCUS AC130947 Accession AC130947
     Fragment Name      Begin     End
     AC130947_0             1    110000
     AC130947_1        100001    210000
     AC130947_2        200001    310000
     AC130947_3        300001    410000
     AC130947_4        400001    496753
Continuation (3 of 5) of AC130947 from base 200001 (AC130947 Rattus norvegicus clone CH2

  Query Match             85.0%;  Score 17;  DB 2;  Length 110000;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TTGCCACTCCCATTCTT 20
              |||||||||||||||||
Db      59683 TTGCCACTCCCATTCTT 59699


RESULT 41
AC026820
LOCUS       AC026820              143454 bp    DNA     linear   HTG 24-MAR-2000
DEFINITION  Homo sapiens chromosome 1 clone RP11-15F19 map 1, WORKING DRAFT
            SEQUENCE, 12 unordered pieces.
ACCESSION   AC026820
VERSION     AC026820.1  GI:7321613
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 143454)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 1, clone RP11-15F19
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 143454)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L7141
                Center clone name: 15_F_19
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 136737 bases at least Q40
                Consensus quality: 140227 bases at least Q30
                Consensus quality: 141337 bases at least Q20
                Insert size: 139000; agarose-fp
                Insert size: 142354; sum-of-contigs
                Quality coverage: 4.4 in Q20 bases; agarose-fp
                Quality coverage: 4.3 in Q20 bases; sum-of-contigs
            --------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 12 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1888: contig of 1888 bp in length
            *     1889     1988: gap of 100 bp
            *     1989     4707: contig of 2719 bp in length
            *     4708     4807: gap of 100 bp
            *     4808     8781: contig of 3974 bp in length
            *     8782     8881: gap of 100 bp
            *     8882    12361: contig of 3480 bp in length
            *    12362    12461: gap of 100 bp
            *    12462    20412: contig of 7951 bp in length
            *    20413    20512: gap of 100 bp
            *    20513    28499: contig of 7987 bp in length
            *    28500    28599: gap of 100 bp
            *    28600    37268: contig of 8669 bp in length
            *    37269    37368: gap of 100 bp
            *    37369    47539: contig of 10171 bp in length
            *    47540    47639: gap of 100 bp
            *    47640    61172: contig of 13533 bp in length
            *    61173    61272: gap of 100 bp
            *    61273    77119: contig of 15847 bp in length
            *    77120    77219: gap of 100 bp
            *    77220   103392: contig of 26173 bp in length
            *   103393   103492: gap of 100 bp
            *   103493   143454: contig of 39962 bp in length.
FEATURES             Location/Qualifiers
     source          1. .143454
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="1"
                     /clone="RP11-15F19"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .1888
                     /note="assembly_fragment"
     misc_feature    1989. .4707
                     /note="assembly_fragment"
     misc_feature    4808. .8781
                     /note="assembly_fragment"
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     misc_feature    8882. .12361
                     /note="assembly_fragment"
     misc_feature    12462. .20412
                     /note="assembly_fragment"
     misc_feature    20513. .28499
                     /note="assembly_fragment"
     misc_feature    28600. .37268
                     /note="assembly_fragment"
     misc_feature    37369. .47539
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    47640. .61172
                     /note="assembly_fragment"
     misc_feature    61273. .77119
                     /note="assembly_fragment"
     misc_feature    77220. .103392
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     misc_feature    103493. .143454
                     /note="assembly_fragment"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 143454;
  Best Local Similarity   100.0%;  Pred. No. 7.2;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db       3978 CATTGCCACTCCCATTC 3994


RESULT 42
AC027556
LOCUS       AC027556               156149 bp    DNA     linear   HTG 04-OCT-2000
DEFINITION  Homo sapiens chromosome 17 clone RP11-81O13 map 17, WORKING DRAFT
            SEQUENCE, 23 unordered pieces.
ACCESSION   AC027556
VERSION     AC027556.2  GI:10567975
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 156149)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-81O13
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 156149)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 4, 2000 this sequence version replaced gi:7342301.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L8949
                Center clone name: 81_O_13
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 94% of reads
                Sequencing vector: Plasmid; n/a; 6% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 144286 bases at least Q40
                Consensus quality: 150098 bases at least Q30
                Consensus quality: 152440 bases at least Q20
                Insert size: 163000; agarose-fp
                Insert size: 153949; sum-of-contigs
                Quality coverage: 4.1 in Q20 bases; agarose-fp
                Quality coverage: 4.3 in Q20 bas.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 23 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     4014: contig of 4014 bp in length
            *     4015     4114: gap of 100 bp
            *     4115     5625: contig of 1511 bp in length
            *     5626     5725: gap of 100 bp
            *     5726     6824: contig of 1099 bp in length
            *     6825     6924: gap of 100 bp
            *     6925     8353: contig of 1429 bp in length
            *     8354     8453: gap of 100 bp
            *     8454     9642: contig of 1189 bp in length
            *     9643     9742: gap of 100 bp
            *     9743    11659: contig of 1917 bp in length
            *    11660    11759: gap of 100 bp
            *    11760    13651: contig of 1892 bp in length
            *    13652    13751: gap of 100 bp
            *    13752    16812: contig of 3061 bp in length
            *    16813    16912: gap of 100 bp
            *    16913    19304: contig of 2392 bp in length
            *    19305    19404: gap of 100 bp
            *    19405    21925: contig of 2521 bp in length
            *    21926    22025: gap of 100 bp
            *    22026    24279: contig of 2254 bp in length
            *    24280    24379: gap of 100 bp
            *    24380    28256: contig of 3877 bp in length
            *    28257    28356: gap of 100 bp
            *    28357    33672: contig of 5316 bp in length
            *    33673    33772: gap of 100 bp
            *    33773    37991: contig of 4219 bp in length
            *    37992    38091: gap of 100 bp
            *    38092    44086: contig of 5995 bp in length
            *    44087    44186: gap of 100 bp
            *    44187    50586: contig of 6400 bp in length
            *    50587    50686: gap of 100 bp
            *    50687    78161: contig of 27475 bp in length
            *    78162    78261: gap of 100 bp
            *    78262    84913: contig of 6652 bp in length
            *    84914    85013: gap of 100 bp
            *    85014    97976: contig of 12963 bp in length
            *    97977    98076: gap of 100 bp
            *    98077   110971: contig of 12895 bp in length
            *   110972   111071: gap of 100 bp
```

```
           *   111072   126745: contig of 15674 bp in length
           *   126746   126845: gap of 100 bp
           *   126846   145802: contig of 18957 bp in length
           *   145803   145902: gap of 100 bp
           *   145903   156149: contig of 10247 bp in length.
FEATURES             Location/Qualifiers
     source          1. .156149
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="17"
                     /map="17"
                     /clone="RP11-81O13"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .4014
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    4115. .5625
                     /note="assembly_fragment"
     misc_feature    5726. .6824
                     /note="assembly_fragment"
     misc_feature    6925. .8353
                     /note="assembly_fragment"
     misc_feature    8454. .9642
                     /note="assembly_fragment"
     misc_feature    9743. .11659
                     /note="assembly_fragment"
     misc_feature    11760. .13651
                     /note="assembly_fragment"
     misc_feature    13752. .16812
                     /note="assembly_fragment"
     misc_feature    16913. .19304
                     /note="assembly_fragment"
     misc_feature    19405. .21925
                     /note="assembly_fragment"
     misc_feature    22026. .24279
                     /note="assembly_fragment"
     misc_feature    24380. .28256
                     /note="assembly_fragment"
     misc_feature    28357. .33672
                     /note="assembly_fragment"
     misc_feature    33773. .37991
                     /note="assembly_fragment"
     misc_feature    38092. .44086
                     /note="assembly_fragment"
     misc_feature    44187. .50586
                     /note="assembly_fragment"
     misc_feature    50687. .78161
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     misc_feature    78262. .84913
                     /note="assembly_fragment"
     misc_feature    85014. .97976
                     /note="assembly_fragment"
     misc_feature    98077. .110971
                     /note="assembly_fragment"
     misc_feature    111072. .126745
                     /note="assembly_fragment"
     misc_feature    126846. .145802
                     /note="assembly_fragment"
     misc_feature    145903. .156149
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 156149;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db      30936 CATTGCCACTCCCATTC 30952
```

```
RESULT 43
AL928688
LOCUS       AL928688              165910 bp    DNA     linear   PRI 27-SEP-2002
DEFINITION  Human DNA sequence from clone RP11-77N10 on chromosome 10, complete
            sequence.
ACCESSION   AL928688
VERSION     AL928688.3  GI:23380957
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 165910)
  AUTHORS   Clark,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 30, 2002 this sequence version replaced gi:23337954.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-77N10 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .165910
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="RP11-77N10"
                     /clone_lib="RPCI-11.1"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 165910;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db     124789 CATTGCCACTCCCATTC 124805


RESULT 44
```

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AL935036
LOCUS       AL935036              166004 bp    DNA     linear   PRI 07-NOV-2002
DEFINITION  Human DNA sequence from clone RP11-257E20 on chromosome 10,
            complete sequence.
ACCESSION   AL935036
VERSION     AL935036.4  GI:24474499
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 166004)
  AUTHORS   Howden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 1, 2002 this sequence version replaced gi:24366850.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 10, constructed by the Sanger Centre Chromosome 10
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr10
            RP11-257E20 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .166004
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="RP11-257E20"
                     /clone_lib="RPCI-11.1"

ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 166004;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db      55282 CATTGCCACTCCCATTC 55298


RESULT 45
AL161734
LOCUS       AL161734              167099 bp    DNA     linear   PRI 10-MAR-2003
DEFINITION  Human DNA sequence from clone RP11-33M22 on chromosome 1q25.2-31.2,
            complete sequence.
ACCESSION   AL161734
VERSION     AL161734.12  GI:28933321
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 167099)
  AUTHORS   Harrison,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Mar 12, 2003 this sequence version replaced gi:15990620.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-33M22 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1. .167099
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="1"
                     /map="q25.2-31.2"
                     /clone="RP11-33M22"
                     /clone_lib="RPCI-11.1"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 167099;
  Best Local Similarity   100.0%;  Pred. No. 7.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CATTGCCACTCCCATTC 18
              |||||||||||||||||
Db      69217 CATTGCCACTCCCATTC 69233


Search completed: August  5, 2005, 01:26:41
Job time : 1833 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 00:40:17 ; Search time 615 Seconds
(without alignments)
210.807 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgccactcccattctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7297361 seqs, 3241162794 residues

Word size : 8

Total number of hits satisfying chosen parameters: 910364

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	US-10-643-801-35	Sequence 35, Appl
c	2	20	100.0	20	21	US-10-643-801-157	Sequence 157, App
c	3	20	100.0	469	16	US-10-116-712-436	Sequence 436, App
c	4	20	100.0	827	14	US-10-121-857-56	Sequence 56, Appl
c	5	20	100.0	827	15	US-10-208-018-56	Sequence 56, Appl
c	6	20	100.0	885	14	US-10-121-857-60	Sequence 60, Appl
c	7	20	100.0	885	15	US-10-208-018-60	Sequence 60, Appl
	8	20	100.0	1030	18	US-10-307-817-539	Sequence 539, App
	9	20	100.0	1077	18	US-10-307-817-538	Sequence 538, App
c	10	20	100.0	1167	9	US-09-794-715A-3	Sequence 3, Appli
c	11	20	100.0	1167	15	US-10-278-733-8	Sequence 8, Appli
c	12	20	100.0	1167	15	US-10-208-018-97	Sequence 97, Appl
c	13	20	100.0	1167	15	US-10-208-018-111	Sequence 111, App
c	14	20	100.0	1167	15	US-10-208-018-126	Sequence 126, App
c	15	20	100.0	1167	15	US-10-046-924-3	Sequence 3, Appli
c	16	20	100.0	1167	16	US-10-286-581-3	Sequence 3, Appli
c	17	20	100.0	1167	17	US-10-446-441-3	Sequence 3, Appli
c	18	20	100.0	1167	21	US-10-945-738-3	Sequence 3, Appli
c	19	20	100.0	1172	18	US-10-307-817-103	Sequence 103, App
c	20	20	100.0	1189	18	US-10-307-817-101	Sequence 101, App
c	21	20	100.0	1189	18	US-10-307-817-107	Sequence 107, App
c	22	20	100.0	1191	18	US-10-307-817-93	Sequence 93, Appl
c	23	20	100.0	1191	18	US-10-307-817-97	Sequence 97, Appl
c	24	20	100.0	1198	18	US-10-307-817-105	Sequence 105, App
c	25	20	100.0	1207	18	US-10-307-817-99	Sequence 99, Appl
c	26	20	100.0	1230	18	US-10-307-817-95	Sequence 95, Appl
c	27	20	100.0	1230	18	US-10-307-817-540	Sequence 540, App
c	28	20	100.0	1231	9	US-09-794-715A-1	Sequence 1, Appli
c	29	20	100.0	1231	15	US-10-046-924-1	Sequence 1, Appli
c	30	20	100.0	1231	16	US-10-286-581-1	Sequence 1, Appli
c	31	20	100.0	1231	17	US-10-446-441-1	Sequence 1, Appli
c	32	20	100.0	1231	21	US-10-945-738-1	Sequence 1, Appli
c	33	20	100.0	1233	15	US-10-046-924-18	Sequence 18, Appl
c	34	20	100.0	1233	16	US-10-286-581-18	Sequence 18, Appl
c	35	20	100.0	1233	21	US-10-945-738-18	Sequence 18, Appl
	36	20	100.0	1510	17	US-10-172-118-2665	Sequence 2665, Ap
	37	20	100.0	1510	18	US-10-342-887-2665	Sequence 2665, Ap
c	38	20	100.0	1570	10	US-09-946-374-291	Sequence 291, App
c	39	20	100.0	1570	13	US-10-052-586-335	Sequence 335, App
c	40	20	100.0	1570	14	US-10-174-590-335	Sequence 335, App
c	41	20	100.0	1570	14	US-10-176-758-335	Sequence 335, App
c	42	20	100.0	1570	14	US-10-175-737-335	Sequence 335, App
c	43	20	100.0	1570	14	US-10-174-581-335	Sequence 335, App
c	44	20	100.0	1570	14	US-10-176-483-335	Sequence 335, App
c	45	20	100.0	1570	14	US-10-176-749-335	Sequence 335, App
c	46	20	100.0	1570	14	US-10-176-914-335	Sequence 335, App
c	47	20	100.0	1570	14	US-10-176-915-335	Sequence 335, App
c	48	20	100.0	1570	14	US-10-173-706-335	Sequence 335, App
c	49	20	100.0	1570	14	US-10-175-738-335	Sequence 335, App
c	50	20	100.0	1570	14	US-10-175-752-335	Sequence 335, App
c	51	20	100.0	1570	14	US-10-176-482-335	Sequence 335, App
c	52	20	100.0	1570	14	US-10-176-757-335	Sequence 335, App
c	53	20	100.0	1570	14	US-10-176-913-335	Sequence 335, App
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c	61	20	100.0	1570	14	US-10-175-739-335	Sequence 335, App
c	62	20	100.0	1570	14	US-10-175-740-335	Sequence 335, App
c	63	20	100.0	1570	14	US-10-175-743-335	Sequence 335, App
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c	66	20	100.0	1570	14	US-10-176-747-335	Sequence 335, App
c	67	20	100.0	1570	14	US-10-176-750-335	Sequence 335, App
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c	69	20	100.0	1570	14	US-10-176-987-335	Sequence 335, App
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c	71	20	100.0	1570	14	US-10-176-993-335	Sequence 335, App
c	72	20	100.0	1570	14	US-10-184-658-335	Sequence 335, App
c	73	20	100.0	1570	14	US-10-176-991-335	Sequence 335, App
c	74	20	100.0	1570	14	US-10-173-695-335	Sequence 335, App
c	75	20	100.0	1570	14	US-10-173-697-335	Sequence 335, App
c	76	20	100.0	1570	14	US-10-173-705-335	Sequence 335, App
c	77	20	100.0	1570	14	US-10-174-576-335	Sequence 335, App
c	78	20	100.0	1570	14	US-10-174-585-335	Sequence 335, App
c	79	20	100.0	1570	14	US-10-174-586-335	Sequence 335, App
c	80	20	100.0	1570	14	US-10-175-747-335	Sequence 335, App

c 81	20	100.0	1570	14	US-10-176-481-335	Sequence 335, App
c 82	20	100.0	1570	14	US-10-176-485-335	Sequence 335, App
c 83	20	100.0	1570	14	US-10-176-487-335	Sequence 335, App
c 84	20	100.0	1570	14	US-10-176-493-335	Sequence 335, App
c 85	20	100.0	1570	14	US-10-176-756-335	Sequence 335, App
c 86	20	100.0	1570	14	US-10-176-911-335	Sequence 335, App
c 87	20	100.0	1570	14	US-10-176-919-335	Sequence 335, App
c 88	20	100.0	1570	14	US-10-176-925-335	Sequence 335, App
c 89	20	100.0	1570	14	US-10-176-978-335	Sequence 335, App
c 90	20	100.0	1570	14	US-10-179-510-335	Sequence 335, App
c 91	20	100.0	1570	14	US-10-180-543-335	Sequence 335, App
c 92	20	100.0	1570	14	US-10-180-544-335	Sequence 335, App
c 93	20	100.0	1570	14	US-10-180-546-335	Sequence 335, App
c 94	20	100.0	1570	14	US-10-180-547-335	Sequence 335, App
c 95	20	100.0	1570	14	US-10-180-549-335	Sequence 335, App
c 96	20	100.0	1570	14	US-10-180-555-335	Sequence 335, App
c 97	20	100.0	1570	14	US-10-180-559-335	Sequence 335, App
c 98	20	100.0	1570	14	US-10-181-000-335	Sequence 335, App
c 99	20	100.0	1570	14	US-10-183-010-335	Sequence 335, App
c 100	20	100.0	1570	14	US-10-183-012-335	Sequence 335, App

ALIGNMENTS

RESULT 1
US-10-643-801-35
; Sequence 35, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-801-35

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 1 GCATTGCCACTCCCATTCTT 20

RESULT 2
US-10-643-801-157/c
; Sequence 157, Application US/10643801
; Publication No. US20050043524A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US
; CURRENT APPLICATION NUMBER: US/10/643,801
; CURRENT FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-643-801-157

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 20 GCATTGCCACTCCCATTCTT 1

RESULT 3
US-10-116-712-436/c
; Sequence 436, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-436

Query Match 100.0%; Score 20; DB 16; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 269 GCATTGCCACTCCCATTCTT 250

RESULT 4
US-10-121-857-56/c
; Sequence 56, Application US/10121857
; Publication No. US20030028923A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.143
; CURRENT APPLICATION NUMBER: US/10/121,857
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 827
; TYPE: DNA
; ORGANISM: Human
US-10-121-857-56

Query Match 100.0%; Score 20; DB 14; Length 827;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 479 GCATTGCCACTCCCATTCTT 460

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RESULT 5
US-10-208-018-56/c
; Sequence 56, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
;  APPLICANT: Lardizabal, Kathryn D
;  APPLICANT:  Hawkins, Deborah J
;  APPLICANT:  Thompson, Gregory A
;  TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
;  FILE REFERENCE: 16515.155
;  CURRENT APPLICATION NUMBER: US/10/208,018
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 10/121,857
;  PRIOR FILING DATE: 2002-04-15
;  PRIOR APPLICATION NUMBER: US 09/345,461
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,631
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 60/130,829
;  PRIOR FILING DATE: 1999-04-23
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
;   LENGTH: 827
;   TYPE: DNA
;   ORGANISM: Human
US-10-208-018-56

  Query Match            100.0%;  Score 20;  DB 15;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        479 GCATTGCCACTCCCATTCTT 460


RESULT 6
US-10-121-857-60/c
; Sequence 60, Application US/10121857
; Publication No. US20030028923A1
; GENERAL INFORMATION:
;  APPLICANT: Lardizabal, Kathryn D
;  APPLICANT:  Hawkins, Deborah J
;  APPLICANT:  Thompson, Gregory A
;  TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
;  FILE REFERENCE: 16515.143
;  CURRENT APPLICATION NUMBER: US/10/121,857
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: US 09/345,461
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,631
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 60/130,829
;  PRIOR FILING DATE: 1999-04-23
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 885
;   TYPE: DNA
;   ORGANISM: murine
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(885)
;   OTHER INFORMATION: unsure at all n locations
US-10-121-857-60

  Query Match            100.0%;  Score 20;  DB 14;  Length 885;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        482 GCATTGCCACTCCCATTCTT 463


RESULT 7
US-10-208-018-60/c
; Sequence 60, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
;  APPLICANT: Lardizabal, Kathryn D
;  APPLICANT:  Hawkins, Deborah J
;  APPLICANT:  Thompson, Gregory A
;  TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
;  FILE REFERENCE: 16515.155
;  CURRENT APPLICATION NUMBER: US/10/208,018
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 10/121,857
;  PRIOR FILING DATE: 2002-04-15
;  PRIOR APPLICATION NUMBER: US 09/345,461
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,631
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 60/130,829
;  PRIOR FILING DATE: 1999-04-23
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 885
;   TYPE: DNA
;   ORGANISM: murine
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(885)
;   OTHER INFORMATION: unsure at all n locations
US-10-208-018-60

  Query Match            100.0%;  Score 20;  DB 15;  Length 885;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        482 GCATTGCCACTCCCATTCTT 463


RESULT 8
US-10-307-817-539
; Sequence 539, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 539
;   LENGTH: 1030
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-307-817-539

  Query Match            100.0%;  Score 20;  DB 18;  Length 1030;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        274 GCATTGCCACTCCCATTCTT 293


RESULT 9
US-10-307-817-538
```

; Sequence 538, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 538
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-307-817-538

Query Match 100.0%; Score 20; DB 18; Length 1077;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 384 GCATTGCCACTCCCATTCTT 403

RESULT 10
US-09-794-715A-3/c
; Sequence 3, Application US/09794715A
; Patent No. US20020119138A1
; GENERAL INFORMATION:
; APPLICANT: Cases, Sylvaine
; APPLICANT: Stone, Scot
; APPLICANT: Zhou, Ping
; APPLICANT: Farese, Robert V.
; TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
; TITLE OF INVENTION: (DGAT2a)
; FILE REFERENCE: 6510240US1
; CURRENT APPLICATION NUMBER: US/09/794,715A
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1137
; OTHER INFORMATION: n = A,T,C or G
US-09-794-715A-3

Query Match 100.0%; Score 20; DB 9; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 698 GCATTGCCACTCCCATTCTT 679

RESULT 11
US-10-278-733-8/c
; Sequence 8, Application US/10278733
; Publication No. US20030100480A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Steven
; APPLICANT: Chen, Hubert
; APPLICANT: Farese, Robert V Jr
; TITLE OF INVENTION: Methods and compositions for modulating
; TITLE OF INVENTION: sebaceous glands
; FILE REFERENCE: UCAL-105CIP4
; CURRENT APPLICATION NUMBER: US/10/278,733
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1167)
; OTHER INFORMATION: Homo sapiens DGAT 2 coding sequence
US-10-278-733-8

Query Match 100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 698 GCATTGCCACTCCCATTCTT 679

RESULT 12
US-10-208-018-97/c
; Sequence 97, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.155
; CURRENT APPLICATION NUMBER: US/10/208,018
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 10/121,857
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
US-10-208-018-97

Query Match 100.0%; Score 20; DB 15; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 698 GCATTGCCACTCCCATTCTT 679

RESULT 13
US-10-208-018-111/c
; Sequence 111, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:

```
;  APPLICANT: Lardizabal, Kathryn D
;  APPLICANT:  Hawkins, Deborah J
;  APPLICANT:  Thompson, Gregory A
;  TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
;  FILE REFERENCE: 16515.155
;  CURRENT APPLICATION NUMBER: US/10/208,018
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 10/121,857
;  PRIOR FILING DATE: 2002-04-15
;  PRIOR APPLICATION NUMBER: US 09/345,461
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,631
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 60/130,829
;  PRIOR FILING DATE: 1999-04-23
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-208-018-111

  Query Match             100.0%;  Score 20;  DB 15;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 14
US-10-208-018-126/c
; Sequence 126, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
;  APPLICANT: Lardizabal, Kathryn D
;  APPLICANT:  Hawkins, Deborah J
;  APPLICANT:  Thompson, Gregory A
;  TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
;  FILE REFERENCE: 16515.155
;  CURRENT APPLICATION NUMBER: US/10/208,018
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: US 10/121,857
;  PRIOR FILING DATE: 2002-04-15
;  PRIOR APPLICATION NUMBER: US 09/345,461
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,631
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: US 60/130,829
;  PRIOR FILING DATE: 1999-04-23
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Murinae gen. sp.
US-10-208-018-126

  Query Match             100.0%;  Score 20;  DB 15;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 15
US-10-046-924-3/c
; Sequence 3, Application US/10046924
; Publication No. US20030124126A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: UCAL240CIP
;  CURRENT APPLICATION NUMBER: US/10/046,924
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1167)
;   OTHER INFORMATION: n = A,T,C or G
US-10-046-924-3

  Query Match             100.0%;  Score 20;  DB 15;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 16
US-10-286-581-3/c
; Sequence 3, Application US/10286581
; Publication No. US20030161831A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang, Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
;  FILE REFERENCE: UCAL240CIP2
;  CURRENT APPLICATION NUMBER: US/10/286,581
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1167)
;   OTHER INFORMATION: n = A,T,C or G
US-10-286-581-3

  Query Match             100.0%;  Score 20;  DB 16;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 17
US-10-446-441-3/c
; Sequence 3, Application US/10446441
; Publication No. US20030202968A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: UCAL-240CON
;  CURRENT APPLICATION NUMBER: US/10/446,441
;  CURRENT FILING DATE:  2003-05-27
;  PRIOR APPLICATION NUMBER: US 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1137
;   OTHER INFORMATION: n = A,T,C or G
US-10-446-441-3

  Query Match            100.0%;  Score 20;  DB 17;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 18
US-10-945-738-3/c
; Sequence 3, Application US/10945738
; Publication No. US20050106697A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
;  FILE REFERENCE: UCAL-240CON2
;  CURRENT APPLICATION NUMBER: US/10/945,738
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 10/286,581
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1167
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1167)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1137
;   OTHER INFORMATION: n = A,T,C or G
US-10-945-738-3

  Query Match            100.0%;  Score 20;  DB 21;  Length 1167;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        698 GCATTGCCACTCCCATTCTT 679


RESULT 19
US-10-307-817-103/c
; Sequence 103, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 103
;   LENGTH: 1172
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)..(1169)
US-10-307-817-103

  Query Match            100.0%;  Score 20;  DB 18;  Length 1172;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        703 GCATTGCCACTCCCATTCTT 684


RESULT 20
US-10-307-817-101/c
; Sequence 101, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 101
;   LENGTH: 1189
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1186)
US-10-307-817-101

  Query Match            100.0%;  Score 20;  DB 18;  Length 1189;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 21
US-10-307-817-107/c
; Sequence 107, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 107
;   LENGTH: 1189
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(1186)
US-10-307-817-107

  Query Match             100.0%;  Score 20;  DB 18;  Length 1189;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 22
US-10-307-817-93/c
; Sequence 93, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 93
;   LENGTH: 1191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1188)
US-10-307-817-93

  Query Match             100.0%;  Score 20;  DB 18;  Length 1191;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        722 GCATTGCCACTCCCATTCTT 703


RESULT 23
US-10-307-817-97/c
; Sequence 97, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 97
;   LENGTH: 1191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1188)
US-10-307-817-97

  Query Match             100.0%;  Score 20;  DB 18;  Length 1191;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        722 GCATTGCCACTCCCATTCTT 703


RESULT 24
US-10-307-817-105/c
; Sequence 105, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 105
;   LENGTH: 1198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)..(1117)
US-10-307-817-105

  Query Match             100.0%;  Score 20;  DB 18;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        711 GCATTGCCACTCCCATTCTT 692


RESULT 25
US-10-307-817-99/c
; Sequence 99, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 99
;   LENGTH: 1207
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1194)
US-10-307-817-99
```

```
  Query Match             100.0%;  Score 20;  DB 18;  Length 1207;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        710 GCATTGCCACTCCCATTCTT 691


RESULT 26
US-10-307-817-95/c
; Sequence 95, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 95
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)..(1168)
US-10-307-817-95

  Query Match             100.0%;  Score 20;  DB 18;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 27
US-10-307-817-540/c
; Sequence 540, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
;  APPLICANT: Agee et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-502C
;  CURRENT APPLICATION NUMBER: US/10/307,817
;  CURRENT FILING DATE:  2002-12-02
;  NUMBER OF SEQ ID NOS: 682
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 540
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-307-817-540

  Query Match             100.0%;  Score 20;  DB 18;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 28
US-09-794-715A-1/c
; Sequence 1, Application US/09794715A
; Patent No. US20020119138A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: 6510240US1
;  CURRENT APPLICATION NUMBER: US/09/794,715A
;  CURRENT FILING DATE:  2001-02-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-794-715A-1

  Query Match             100.0%;  Score 20;  DB 9;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 29
US-10-046-924-1/c
; Sequence 1, Application US/10046924
; Publication No. US20030124126A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: UCAL240CIP
;  CURRENT APPLICATION NUMBER: US/10/046,924
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-046-924-1

  Query Match             100.0%;  Score 20;  DB 15;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 30
US-10-286-581-1/c
; Sequence 1, Application US/10286581
; Publication No. US20030161831A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang, Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
```

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;  FILE REFERENCE: UCAL240CIP2
;  CURRENT APPLICATION NUMBER: US/10/286,581
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-286-581-1

  Query Match             100.0%;  Score 20;  DB 16;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 31
US-10-446-441-1/c
; Sequence 1, Application US/10446441
; Publication No. US20030202968A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: UCAL-240CON
;  CURRENT APPLICATION NUMBER: US/10/446,441
;  CURRENT FILING DATE:  2003-05-27
;  PRIOR APPLICATION NUMBER: US 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-446-441-1

  Query Match             100.0%;  Score 20;  DB 17;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 32
US-10-945-738-1/c
; Sequence 1, Application US/10945738
; Publication No. US20050106697A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
;  FILE REFERENCE: UCAL-240CON2
;  CURRENT APPLICATION NUMBER: US/10/945,738
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 10/286,581
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-945-738-1

  Query Match             100.0%;  Score 20;  DB 21;  Length 1231;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        702 GCATTGCCACTCCCATTCTT 683


RESULT 33
US-10-046-924-18/c
; Sequence 18, Application US/10046924
; Publication No. US20030124126A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
;  TITLE OF INVENTION:  (DGAT2a)
;  FILE REFERENCE: UCAL240CIP
;  CURRENT APPLICATION NUMBER: US/10/046,924
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1233
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-046-924-18

  Query Match             100.0%;  Score 20;  DB 15;  Length 1233;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        705 GCATTGCCACTCCCATTCTT 686


RESULT 34
US-10-286-581-18/c
; Sequence 18, Application US/10286581
; Publication No. US20030161831A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
```

```
;  APPLICANT:  Chi-Liang, Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
;  FILE REFERENCE: UCAL240CIP2
;  CURRENT APPLICATION NUMBER: US/10/286,581
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1233
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-286-581-18

  Query Match           100.0%;  Score 20;  DB 16;  Length 1233;
  Best Local Similarity  100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        705 GCATTGCCACTCCCATTCTT 686


RESULT 35
US-10-945-738-18/c
; Sequence 18, Application US/10945738
; Publication No. US20050106697A1
; GENERAL INFORMATION:
;  APPLICANT: Cases, Sylvaine
;  APPLICANT:  Stone, Scot
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Farese, Robert V.
;  APPLICANT:  Chi-Liang Eric Yen
;  TITLE OF INVENTION: Mono- and diacyglycerol acyltransferases
;  TITLE OF INVENTION:  and methods of use thereof
;  FILE REFERENCE: UCAL-240CON2
;  CURRENT APPLICATION NUMBER: US/10/945,738
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 10/286,581
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: 60/271,307
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 09/794,715
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 10/046,924
;  PRIOR FILING DATE: 2002-01-14
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1233
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-945-738-18

  Query Match           100.0%;  Score 20;  DB 21;  Length 1233;
  Best Local Similarity  100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        705 GCATTGCCACTCCCATTCTT 686


RESULT 36
US-10-172-118-2665
; Sequence 2665, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Chris
;  APPLICANT:  Van 't Veer, Laura
;  APPLICANT:  Van de Vijver, Marc
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-999
;  CURRENT APPLICATION NUMBER: US/10/172,118
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2665
;   LENGTH: 1510
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Contig58260
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2665

  Query Match           100.0%;  Score 20;  DB 17;  Length 1510;
  Best Local Similarity  100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       1491 GCATTGCCACTCCCATTCTT 1510


RESULT 37
US-10-342-887-2665
; Sequence 2665, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2665
;   LENGTH: 1510
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-2665

  Query Match           100.0%;  Score 20;  DB 18;  Length 1510;
  Best Local Similarity  100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db       1491 GCATTGCCACTCCCATTCTT 1510
```

RESULT 38
US-09-946-374-291/c
; Sequence 291, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484

; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 20; DB 10; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        882 GCATTGCCACTCCCATTCTT 863
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RESULT 39
US-10-052-586-335/c
; Sequence 335, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
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; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
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; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
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; PRIOR APPLICATION NUMBER: 60/082797
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
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; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-18
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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 20; DB 13; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCATTGCCACTCCCATTCTT 20
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Db        882 GCATTGCCACTCCCATTCTT 863
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RESULT 40
US-10-174-590-335/c
; Sequence 335, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.

```
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
;   LENGTH: 1570
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-174-590-335

  Query Match            100.0%;  Score 20;  DB 14;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 41
US-10-176-758-335/c
; Sequence 335, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
;   LENGTH: 1570
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-176-758-335

  Query Match            100.0%;  Score 20;  DB 14;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 42
US-10-175-737-335/c
; Sequence 335, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C50
;  CURRENT APPLICATION NUMBER: US/10/175,737
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
;   LENGTH: 1570
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-175-737-335

  Query Match            100.0%;  Score 20;  DB 14;  Length 1570;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        882 GCATTGCCACTCCCATTCTT 863


RESULT 43
US-10-174-581-335/c
; Sequence 335, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C41
;  CURRENT APPLICATION NUMBER: US/10/174,581
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: 10/052586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
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;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
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;  PRIOR APPLICATION NUMBER: 60/063564
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063734
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063870
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; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
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; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
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; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105

; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 44
US-10-176-483-335/c
; Sequence 335, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-335

Query Match 100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 882 GCATTGCCACTCCCATTCTT 863

RESULT 45
US-10-176-749-335/c
; Sequence 335, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 335
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-335

Query Match 100.0%; Score 20; DB 14; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 882 GCATTGCCACTCCCATTCTT 863

Search completed: August 5, 2005, 02:33:27
Job time : 621 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 16:53:28 ; Search time 3141 Seconds
(without alignments)
242.370 Million cell updates/sec

Title: US-10-643-801A-35
Perfect score: 20
Sequence: 1 gcattgccactcccattctt 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 8

Total number of hits satisfying chosen parameters: 6604802

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	288	2	BF236347	BF236347 602025981
c 2	20	100.0	291	4	BG687855	BG687855 335149 BA
c 3	20	100.0	293	7	H25606	H25606 yl48c07.r1
c 4	20	100.0	300	4	BG190696	BG190696 RST9770 A
5	20	100.0	324	9	CE638239	CE638239 tigr-gss-
c 6	20	100.0	415	1	AA674642	AA674642 vq02a10.r
c 7	20	100.0	421	2	BF430191	BF430191 256153 MA
c 8	20	100.0	426	2	BF147241	BF147241 uw67f05.y
c 9	20	100.0	435	7	R69540	R69540 yj82e11.r1
c 10	20	100.0	450	1	AA880955	AA880955 vx34c06.r
c 11	20	100.0	466	1	AA797343	AA797343 vw23h05.r
c 12	20	100.0	502	2	BE482224	BE482224 167934 BA
c 13	20	100.0	503	6	CA536347	CA536347 C0233B11-
c 14	20	100.0	508	2	BE479873	BE479873 164726 BA
c 15	20	100.0	511	4	BG741469	BG741469 602632261
c 16	20	100.0	534	2	BE625643	BE625643 ut98b12.y
c 17	20	100.0	540	2	BE014044	BE014044 125617 MA
c 18	20	100.0	559	4	BM851596	BM851596 K-EST0132
c 19	20	100.0	586	7	CF106297	CF106297 maj05c07.
c 20	20	100.0	590	4	BG696693	BG696693 602659709
c 21	20	100.0	592	5	BP316675	BP316675 BP316675
c 22	20	100.0	615	5	BP382116	BP382116 BP382116
c 23	20	100.0	621	7	CK970536	CK970536 4086279 B
c 24	20	100.0	625	4	BG484381	BG484381 602505020
c 25	20	100.0	631	2	BF660115	BF660115 maa27g08.
c 26	20	100.0	632	6	CA535709	CA535709 C0223B02-
c 27	20	100.0	646	6	CB267111	CB267111 1006017 H
c 28	20	100.0	653	4	BI144404	BI144404 602908548
c 29	20	100.0	663	4	BI908609	BI908609 603066720
c 30	20	100.0	677	2	BF237046	BF237046 602026681
c 31	20	100.0	698	2	BF236900	BF236900 602026519
c 32	20	100.0	710	4	BI332607	BI332607 602980747
c 33	20	100.0	718	4	BI915586	BI915586 603176945
c 34	20	100.0	732	4	BG695886	BG695886 602657850
c 35	20	100.0	743	4	BG194285	BG194285 RST13430
c 36	20	100.0	743	4	BG695953	BG695953 602657968
c 37	20	100.0	747	7	CR383515	CR383515 CR383515
38	20	100.0	762	4	BF980113	BF980113 602288115
c 39	20	100.0	776	4	BG739895	BG739895 602630838
c 40	20	100.0	781	4	BG697487	BG697487 602660680
c 41	20	100.0	789	4	BG189090	BG189090 RST8128 A
c 42	20	100.0	800	4	BG212376	BG212376 RST31963
c 43	20	100.0	800	4	BG865428	BG865428 602783545
c 44	20	100.0	809	4	BI247050	BI247050 602960387
c 45	20	100.0	816	5	BU541989	BU541989 AGENCOURT
c 46	20	100.0	817	4	BI145888	BI145888 602911193
c 47	20	100.0	819	5	BU939162	BU939162 AGENCOURT
c 48	20	100.0	822	5	BU422455	BU422455 603230757
c 49	20	100.0	857	4	BG681732	BG681732 602627853
c 50	20	100.0	890	4	BM044041	BM044041 603621091
c 51	20	100.0	897	4	BG740407	BG740407 602634184
c 52	20	100.0	921	2	BF235987	BF235987 602025672
c 53	20	100.0	930	6	CB201584	CB201584 AGENCOURT
c 54	20	100.0	985	4	BI257050	BI257050 602978893
c 55	20	100.0	1021	5	BM922778	BM922778 AGENCOURT
c 56	20	100.0	1167	9	AY413823	AY413823 Homo sapi
c 57	20	100.0	1167	9	AY413825	AY413825 Mus muscu
c 58	20	100.0	1458	3	AK016660	AK016660 Mus muscu
c 59	20	100.0	2262	3	AK002443	AK002443 Mus muscu
c 60	20	100.0	5929	3	CR749377	CR749377 Homo sapi
c 61	19	95.0	343	4	BG694175	BG694175 345227 BA
c 62	19	95.0	955	4	BI329751	BI329751 602985095
c 63	19	95.0	1068	5	BU432841	BU432841 603222475
c 64	18	90.0	648	4	BI148931	BI148931 602908974
c 65	18	90.0	802	5	BU240541	BU240541 603321673
c 66	17	85.0	328	6	CB544923	CB544923 AMGNNUC;S
c 67	17	85.0	400	5	BP074578	BP074578 BP074578
c 68	17	85.0	412	5	BP070330	BP070330 BP070330
c 69	17	85.0	436	5	BP048604	BP048604 BP048604
c 70	17	85.0	480	5	BP057725	BP057725 BP057725
c 71	17	85.0	508	5	BP032369	BP032369 BP032369
c 72	17	85.0	522	5	BP050447	BP050447 BP050447
c 73	17	85.0	609	9	CL360447	CL360447 RPCI44_33
c 74	17	85.0	737	6	CA254078	CA254078 SCRLFL410
75	17	85.0	858	9	CC542723	CC542723 CH240_424
c 76	16	80.0	253	8	AZ222991	AZ222991 RPCI-23-9
77	16	80.0	376	8	BH832646	BH832646 BACPP35-F
78	16	80.0	441	6	BY646381	BY646381 BY646381
c 79	16	80.0	524	5	BQ623490	BQ623490 USDA-FP_0
c 80	16	80.0	568	9	FR0024959	AL017799 F.rubripe
81	16	80.0	588	5	BQ488822	BQ488822 89-E8455-
c 82	16	80.0	654	1	AL869177	AL869177 AL869177
c 83	16	80.0	658	1	AL655054	AL655054 AL655054
c 84	16	80.0	686	9	AG066546	AG066546 Pan trogl
c 85	16	80.0	689	9	AG086766	AG086766 Pan trogl
c 86	16	80.0	705	7	CF176858	CF176858 805279 MA
c 87	16	80.0	798	7	CN277508	CN277508 170004180
c 88	16	80.0	800	4	BG199398	BG199398 RST18681
c 89	16	80.0	843	9	CL944456	CL944456 OsIFSB003
c 90	16	80.0	865	4	BI757445	BI757445 603029383
c 91	16	80.0	983	5	BQ649756	BQ649756 AGENCOURT
c 92	16	80.0	983	7	CR293208	CR293208 CR293208
93	16	80.0	1071	5	BM906576	BM906576 AGENCOURT
94	16	80.0	1684	4	BG028155	BG028155 602293217
c 95	15	75.0	174	1	AI834935	AI834935 UI-M-AN1-
96	15	75.0	192	2	BB213350	BB213350 BB213350
97	15	75.0	227	7	N54232	N54232 yz03g01.r1

98	15	75.0	238	6	CA909075	CA909075	PCSC07883
99	15	75.0	268	6	CA909073	CA909073	PCS04651
100	15	75.0	273	2	BB373219	BB373219	BB373219

ALIGNMENTS

RESULT 1
BF236347/c
LOCUS BF236347 288 bp mRNA linear EST 14-NOV-2000
DEFINITION 602025981F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4160948 5', mRNA sequence.
ACCESSION BF236347
VERSION BF236347.1 GI:11149879
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 288)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9441 row: b column: 21
High quality sequence stop: 288.
FEATURES Location/Qualifiers
source 1. .288
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4160948"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 82 GCATTGCCACTCCCATTCTT 63

RESULT 2
BG687855/c
LOCUS BG687855 291 bp mRNA linear EST 27-MAR-2003
DEFINITION 335149 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG687855
VERSION BG687855.1 GI:13929656
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 291)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P., Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and Quackenbush,J.
TITLE Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index
JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
PUBMED 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 33 row: M column: 14
Seq primer: ATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .291
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 239 GCATTGCCACTCCCATTCTT 220

RESULT 3
H25606/c
LOCUS H25606 293 bp mRNA linear EST 10-JUL-1995
DEFINITION yl48c07.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161484 5', mRNA sequence.
ACCESSION H25606
VERSION H25606.1 GI:894729
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 293)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 676
High quality sequence stops: 260
Source: IMAGE Consortium, LLNL

```
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 676   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 260.
FEATURES              Location/Qualifiers
     source           1. .293
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="GDB:575637"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:161484"
                      /sex="Female"
                      /dev_stage="adult"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares breast 3NbHBst"
                      /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                      Library went through one round of normalization to a Cot =
                      20. Library constructed by Bento Soares and M.Fatima
                      Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 293;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db         20 GCATTGCCACTCCCATTCTT 1


RESULT 4
BG190696/c
LOCUS       BG190696                300 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST9770 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG190696
VERSION     BG190696.1  GI:13712383
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 250.
FEATURES              Location/Qualifiers
     source           1. .300
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /cell_line="HT1080"
                      /clone_lib="Athersys RAGE Library"
                      /note="See 'Creation of Genome-wide Protein Expression
                      Libraries using Random Activation of Gene Expression',
                      Nature Biotechnology, in press. Note that even though the
                      cell type indicated is HT1080, since a random activation
                      method was used, these sequence tags are not necessarily
                      expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        262 GCATTGCCACTCCCATTCTT 243


RESULT 5
CE638239
LOCUS       CE638239                324 bp    DNA     linear   GSS 29-SEP-2003
DEFINITION  tigr-gss-dog-17000366770212 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE638239
VERSION     CE638239.1  GI:36955821
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .324
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /strain="Standard Poodle"
                      /db_xref="taxon:9615"
                      /clone_lib="Dog Library"
                      /note="Site_1: BstXI; Libraries were prepared from
                      peripheral blood"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 0.36;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db         74 GCATTGCCACTCCCATTCTT 93


RESULT 6
AA674642/c
LOCUS       AA674642                415 bp    mRNA    linear   EST 28-NOV-1997
DEFINITION  vq02a10.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:1093050 5', mRNA sequence.
ACCESSION   AA674642
VERSION     AA674642.1  GI:2651879
KEYWORDS    EST.
```

```
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:599282
            Seq primer: -28m13 rev1 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1093050"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        293 GCATTGCCACTCCCATTCTT 274


RESULT 7
BF430191/c
LOCUS       BF430191                421 bp    mRNA    linear   EST 29-NOV-2000
DEFINITION  256153 MARC BSM Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BF430191
VERSION     BF430191.1  GI:11442288
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Warren,W.C., Tao,N., Allison,T., Wagner,S., Mathialagan,N.,
            Kata,S., Johnson,J., Smith,T.P.L. and Womack,J.
  TITLE     A survey of genes transcribed in bovine skeletal muscle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: GGAAACAGCTATGACCATG
            BACKWARD: GTTTTCCCAGTCACGAC
            Seq primer: AATTAACCCTCACTAAAGGG.
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="Skeletal muscle"
                     /lab_host="XLOLR"
                     /clone_lib="MARC BSM"
                     /note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
                     Library obtained from Stratagene, catalog #937721. Library
                     made from skeletal muscle of a two year old Holstein cow."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 421;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        131 GCATTGCCACTCCCATTCTT 112


RESULT 8
BF147241/c
LOCUS       BF147241                426 bp    mRNA    linear   EST 26-OCT-2000
DEFINITION  uw67f05.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:3467073 5' similar to TR:O74850 O74850 HYPOTHETICAL 25.8 KD
            PROTEIN ;, mRNA sequence.
ACCESSION   BF147241
VERSION     BF147241.1  GI:11028636
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Other_ESTs: uw67f05.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1386433
            Seq primer: -40RP from Gibco
            High quality sequence stop: 344.
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3467073"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded  cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I  and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is normalized.  Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
```

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ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 426;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        347 GCATTGCCACTCCCATTCTT 328


RESULT 9
R69540/c
LOCUS       R69540                   435 bp    mRNA    linear   EST 01-JUN-1995
DEFINITION  yj82e11.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155276 5', mRNA sequence.
ACCESSION   R69540
VERSION     R69540.1  GI:843057
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 905
            High quality sequence stops: 350
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 905   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 350.
FEATURES             Location/Qualifiers
     source          1. .435
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:571443"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155276"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares breast 2NbHBst"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db         20 GCATTGCCACTCCCATTCTT 1


RESULT 10
AA880955/c
LOCUS       AA880955                 450 bp    mRNA    linear   EST 26-MAR-1998
DEFINITION  vx34c06.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone
            IMAGE:1277098 5' similar to WP:W01A11.2 CE14392 ;, mRNA sequence.
ACCESSION   AA880955
VERSION     AA880955.1  GI:2989938
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:668898
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 435.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6 x CBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1277098"
                     /sex="female"
                     /tissue_type="lung"
                     /dev_stage="6-8 month old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene mouse lung 937302"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. 6-8 month old female lung and 1.5 year old male
                     lung were source of mRNA. Average insert size: 1.5 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        166 GCATTGCCACTCCCATTCTT 147


RESULT 11
AA797343/c
LOCUS       AA797343                 466 bp    mRNA    linear   EST 10-FEB-1998
DEFINITION  vw23h05.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
            IMAGE:1244697 5' similar to TR:O01881 O01881 COSMID K07B1. ;, mRNA
            sequence.
ACCESSION   AA797343
VERSION     AA797343.1  GI:2860298
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KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:658385
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .466
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1244697"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NbMMG"
                     /note="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 466;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        201 GCATTGCCACTCCCATTCTT 182


RESULT 12
BE482224/c
LOCUS       BE482224                502 bp    mRNA    linear   EST 27-MAR-2003
DEFINITION  167934 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE482224
VERSION     BE482224.1  GI:9601757
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
  TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
  JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
  MEDLINE   22135956
   PUBMED   12140684
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@lpsi.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 22  row: P  column: 6
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="BARC 5BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        482 GCATTGCCACTCCCATTCTT 463


RESULT 13
CA536347/c
LOCUS       CA536347                503 bp    mRNA    linear   EST 19-NOV-2002
DEFINITION  C0233B11-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus
            musculus cDNA clone NIA:C0233B11 IMAGE:30013750 5', mRNA sequence.
ACCESSION   CA536347
VERSION     CA536347.1  GI:25075618
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 503)
  AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Tanaka,T., Lim,M.K.,
            Luo,A. and Ko,M.S.H.
  TITLE     Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
            (Long)
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: C0233B11-3
            Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: C0233  row: B  column: 11
            Seq primer: M13 Reverse
            High quality sequence stop: 503
```

```
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .503
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:C0233B11-5N"
                     /db_xref="taxon:10090"
                     /clone="NIA:C0233B11 IMAGE:30013750"
                     /tissue_type="whole embryo including extraembryonic
                     tissues at 7.5-days postcoitum"
                     /dev_stage="7.5-days postcoitum"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
                     (Long)"
                     /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
                     NotI; Mouse cDNA project by the Laboratory of Genetics,
                     National Institute on Aging (NIA), Intramural Research
                     Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                     a long-transcript enriched cDNA library (Ref. Genome Res.
                     11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                     extracted from a pool of four embryos at 7.5-days
                     postcoitum. Double-stranded cDNAs were synthesized with an
                     Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT-3'] from
                     7 ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pSPORT1 plasmid vector.
                     The DH10B E. coli host was transformed with the ligation
                     mixture by the standard chemical method. The average
                     insert size is about 2.2 kb. The library was constructed
                     by Yulan Piao (NIA)."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        455 GCATTGCCACTCCCATTCTT 436


RESULT 14
BE479873/c
LOCUS       BE479873                508 bp    mRNA    linear   EST 27-MAR-2003
DEFINITION  164726 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE479873
VERSION     BE479873.1  GI:9599406
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
  TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
  JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
  MEDLINE   22135956
   PUBMED   12140684
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@lpsi.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 14  row: J  column: 14
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="BARC 5BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        164 GCATTGCCACTCCCATTCTT 145


RESULT 15
BG741469/c
LOCUS       BG741469                511 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602632261F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4777455 5',
            mRNA sequence.
ACCESSION   BG741469
VERSION     BG741469.1  GI:14052122
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 511)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10631  row: j  column: 16
            High quality sequence stop: 509.
FEATURES             Location/Qualifiers
     source          1. .511
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4777455"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 511;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        105 GCATTGCCACTCCCATTCTT 86


RESULT 16
BE625643/c
LOCUS       BE625643                534 bp    mRNA    linear   EST 24-AUG-2000
DEFINITION  ut98b12.y2 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:3370463 5' similar to WP:K07B1.4 CE11882 ;, mRNA sequence.
ACCESSION   BE625643
VERSION     BE625643.1  GI:9906137
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1080067
            Seq primer: -40RP from Gibco
            High quality sequence stop: 479.
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3370463"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from mammary
                     gland tissue from a lactating female, and was then primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library is normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db         47 GCATTGCCACTCCCATTCTT 28


RESULT 17
BE014044/c
LOCUS       BE014044                540 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  125617 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE014044
VERSION     BE014044.1  GI:8275035
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 54  row: C  column: 20
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 1PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        537 GCATTGCCACTCCCATTCTT 518


RESULT 18
BM851596/c
LOCUS       BM851596                559 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0132503 S21SNU520 Homo sapiens cDNA clone S21SNU520-34-H10 5',
            mRNA sequence.
ACCESSION   BM851596
VERSION     BM851596.1  GI:19207995
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 559)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 34  row: H  column: 10
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            High quality sequence stop: 559.
FEATURES             Location/Qualifiers
     source          1. .559
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S21SNU520-34-H10"
                     /sex="F"
                     /tissue_type="Stomach"
                     /cell_type="Floating aggregates"
                     /cell_line="SNU-520"
                     /lab_host="Top10F'"
                     /clone_lib="S21SNU520"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        118 GCATTGCCACTCCCATTCTT 99


RESULT 19
CF106297/c
LOCUS       CF106297                586 bp    mRNA    linear   EST 22-JUL-2003
DEFINITION  maj05c07.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone
            IMAGE:6927543 5' similar to TR:Q9UDW7 Q9UDW7 WUGSC:H_DJ0747G18.5
            PROTEIN ;, mRNA sequence.
ACCESSION   CF106297
VERSION     CF106297.1  GI:33145364
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
            Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
            Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
            Bennett,J., Waterston,R. and Wilson,R.
  TITLE     NIEHS Mouse
  JOURNAL   Unpublished (2002)
COMMENT     Contact: McCarrey/Eddy NIEHS Mouse
            NIEHS Mouse
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed and donated by J. McCarrey, Ph.D. (Southwest
            Foundation for Biomedical Research, Dept. of Genetics) - excision
            done by E.M. Eddy, Ph.D. (National Institutes of Health, National
            Institute of Environmental Health Sciences).
            MGI:2498328
            Seq primer: Primer name ambiguous.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6927543"
                     /sex="male"
                     /tissue_type="round spermatids, pooled from multiple mice"
                     /dev_stage="60 day"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="McCarrey Eddy round spermatid"
                     /note="Organ: testis; Vector: pBluescript SK+
                     (Stratagene); Site_1: XhoII; Site_2: EcoRI; cDNA oligo
                     dT-primed [5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTT-3'] and
                     directionally cloned  using 5' linkers 5'-AATTCGGCACGAG-3'
                     and 5'-CTCGTGCCG-3'. Size selection of >400bp material
                     gives average insert size ranging from 1-2 kb. Library was
                     mass excised (from  lambda-UniZAP-XR) and resulting
                     single-stranded phagemids were prepped and tranformed
                     into DH10B. Library contains 98.5% recombinants.
                     References: J. Androl. 20:635-639 and Gene 25:263-269.
                     Library constructed and donated by J. McCarrey, Ph.D.
                     (Southwest Foundation for Biomedical Research, Dept. of
                     Genetics); excision done by E.M. Eddy, Ph.D. (National
                     Institutes of  Health, National Institute of Environmental
                     Health Sciences).  Original lambda-based library is
                     available through ATCC, catalog #63423."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        108 GCATTGCCACTCCCATTCTT 89


RESULT 20
BG696693/c
LOCUS       BG696693                590 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602659709F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802594 5',
            mRNA sequence.
ACCESSION   BG696693
VERSION     BG696693.1  GI:13962102
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10697  row: b  column: 03
            High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4802594"
                     /lab_host="DH10B (T1 phage-resistant)"
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                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        186 GCATTGCCACTCCCATTCTT 167


RESULT 21
BP316675/c
LOCUS       BP316675                 592 bp    mRNA    linear   EST 17-SEP-2004
DEFINITION  BP316675 Sugano cDNA library, pericardium Homo sapiens cDNA clone
            PCD01990, mRNA sequence.
ACCESSION   BP316675
VERSION     BP316675.1  GI:52245650
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="PCD01990"
                     /tissue_type="pericardium"
                     /clone_lib="Sugano cDNA library, pericardium"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 5;  Length 592;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        159 GCATTGCCACTCCCATTCTT 140


RESULT 22
BP382116/c
LOCUS       BP382116                 615 bp    mRNA    linear   EST 21-SEP-2004
DEFINITION  BP382116 Sugano cDNA library, adipose tissue Homo sapiens cDNA
            clone adSE01532, mRNA sequence.
ACCESSION   BP382116
VERSION     BP382116.1  GI:52417687
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .615
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="adSE01532"
                     /tissue_type="adipose tissue"
                     /clone_lib="Sugano cDNA library, adipose tissue"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 5;  Length 615;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        221 GCATTGCCACTCCCATTCTT 202


RESULT 23
CK970536/c
LOCUS       CK970536                 621 bp    mRNA    linear   EST 16-MAR-2004
DEFINITION  4086279 BARC 9BOV Bos taurus cDNA clone 9BOV31_D16 5', mRNA
            sequence.
ACCESSION   CK970536
VERSION     CK970536.1  GI:45488510
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
  TITLE     Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt " -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 31  row: D  column: 16
            Seq primer: CCCAGTCACGACGTTGTAAAACG
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="9BOV31_D16"
                     /sex="Male"
                     /tissue_type="Pooled"
                     /dev_stage="Multiple"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="BARC 9BOV"
                     /note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
                     Site_2: NotI; Equimolar amounts of mRNA extracted from
```

fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 621;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 510 GCATTGCCACTCCCATTCTT 491

RESULT 24
BG484381/c
LOCUS BG484381 625 bp mRNA linear EST 21-MAR-2001
DEFINITION 602505020F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618421 5', mRNA sequence.
ACCESSION BG484381
VERSION BG484381.1 GI:13416660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 625)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1376 row: h column: 06
High quality sequence stop: 624.
FEATURES Location/Qualifiers
source 1. .625
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4618421"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 438 GCATTGCCACTCCCATTCTT 419

RESULT 25
BF660115/c
LOCUS BF660115 631 bp mRNA linear EST 20-DEC-2000
DEFINITION maa27g08.y1 NCI_CGAP_Li10 Mus musculus cDNA clone IMAGE:3812534 5' similar to TR:Q9UDW7 Q9UDW7 WUGSC:H_DJ0747G18.5 PROTEIN ;, mRNA sequence.
ACCESSION BF660115
VERSION BF660115.1 GI:11925249
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 631)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: maa27g08.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

MGI:1454646
Seq primer: -40RP from Gibco
High quality sequence stop: 437.
FEATURES Location/Qualifiers
source 1. .631
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3812534"
/sex="female"
/dev_stage="10 weeks"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li10"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Library constructed by Life Technologies."
ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 240 GCATTGCCACTCCCATTCTT 221

RESULT 26
CA535709/c
LOCUS CA535709 632 bp mRNA linear EST 18-NOV-2002
DEFINITION C0223B02-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:C0223B02 IMAGE:30012781 5', mRNA sequence.
ACCESSION CA535709
VERSION CA535709.1 GI:25069331
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Tanaka,T., Lim,M.K., Luo,A. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Contact: Dawood B. Dudekula

```
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: C0223  row: B  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 632
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .632
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="niaEST:C0223B02-5N"
                      /db_xref="taxon:10090"
                      /clone="NIA:C0223B02 IMAGE:30012781"
                      /tissue_type="whole embryo including extraembryonic
                      tissues at 7.5-days postcoitum"
                      /dev_stage="7.5-days postcoitum"
                      /lab_host="DH10B"
                      /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
                      (Long)"
                      /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
                      NotI; Mouse cDNA project by the Laboratory of Genetics,
                      National Institute on Aging (NIA), Intramural Research
                      Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                      a long-transcript enriched cDNA library (Ref. Genome Res.
                      11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                      extracted from a pool of four embryos at 7.5-days
                      postcoitum. Double-stranded cDNAs were synthesized with an
                      Oligo(dT) primer [Invitrogen:
                      5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                      7 ug of total RNA, treated with T4 DNA polymerase, and
                      purified by ethanol-precipitation. The cDNAs were ligated
                      to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                      separated from free linkers by Centricon 100. Then, the
                      cDNAs were amplified by long-range high fidelity PCR using
                      Ex Taq polymerase (Takara) with a primer Sal4-S. The
                      products were purified by phenol/chloroform and Centricon
                      100. The cDNAs were digested with SalI and NotI enzymes
                      and cloned into SalI/NotI site of pSPORT1 plasmid vector.
                      The DH10B E. coli host was transformed with the ligation
                      mixture by the standard chemical method. The average
                      insert size is about 2.2 kb. The library was constructed
                      by Yulan Piao (NIA)."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        455 GCATTGCCACTCCCATTCTT 436


RESULT 27
CB267111/c
LOCUS       CB267111                646 bp    mRNA    linear   EST 20-FEB-2003
DEFINITION  1006017 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
            cDNA 5', mRNA sequence.
ACCESSION   CB267111
VERSION     CB267111.1  GI:28441697
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
  TITLE     EST analysis of human adipose gene expression
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Gong Da-Wei
            Division of Endocrinology, Diabetes and Nutrition
            University of Maryland
            660 Redwood St, HH497, Baltimore, MD 21201, USA
            Tel: 410 706 1672
            Fax: 410 706 1622
            Email: dgong@medicine.umaryland.edu
            PCR PRimers
            FORWARD: CTCGGGAAGCGCGCCATTGTGTTGGT
            BACKWARD: AATACGACTCACTATAGGGCGAATTGG
            Seq primer: GTTGGTACCCGGGAATTC.
FEATURES              Location/Qualifiers
     source           1. .646
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /sex="Male and Female"
                      /tissue_type="Adipose"
                      /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
                      /note="Vector: lambdaTriplEx"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 646;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        223 GCATTGCCACTCCCATTCTT 204


RESULT 28
BI144404/c
LOCUS       BI144404                653 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  602908548F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5049851 5',
            mRNA sequence.
ACCESSION   BI144404
VERSION     BI144404.1  GI:14604405
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11135  row: p  column: 12
            High quality sequence stop: 653.
FEATURES              Location/Qualifiers
     source           1. .653
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="FVB/N"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:5049851"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Li9"
                      /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                      Average insert size 1.9 kb. Constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 653;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        507 GCATTGCCACTCCCATTCTT 488


RESULT 29
BI908609/c
LOCUS       BI908609                663 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603066720F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215900 5',
            mRNA sequence.
ACCESSION   BI908609
VERSION     BI908609.1  GI:16171624
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11542  row: g  column: 05
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5215900"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 663;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        537 GCATTGCCACTCCCATTCTT 518


RESULT 30
BF237046/c
LOCUS       BF237046                677 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  602026681F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4161717 5',
            mRNA sequence.
ACCESSION   BF237046
VERSION     BF237046.1  GI:11150963
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9443  row: b  column: 22
            High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source          1. .677
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4161717"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Li9"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 2;  Length 677;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        342 GCATTGCCACTCCCATTCTT 323


RESULT 31
BF236900/c
LOCUS       BF236900                698 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  602026519F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4161773 5',
            mRNA sequence.
ACCESSION   BF236900
VERSION     BF236900.1  GI:11150817
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9443  row: e  column: 06
            High quality sequence stop: 691.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4161773"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 465 GCATTGCCACTCCCATTCTT 446

RESULT 32
BI332607/c
LOCUS BI332607 710 bp mRNA linear EST 30-JUL-2001
DEFINITION 602980747F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5133874 5', mRNA sequence.
ACCESSION BI332607
VERSION BI332607.1 GI:15017264
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 710)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11328 row: m column: 11
High quality sequence start: 8
High quality sequence stop: 701.
FEATURES Location/Qualifiers
source 1. .710
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5133874"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 710;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
||||||||||||||||||||
Db 496 GCATTGCCACTCCCATTCTT 477

RESULT 33
BI915586/c
LOCUS BI915586 718 bp mRNA linear EST 16-OCT-2001
DEFINITION 603176945F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241299 5', mRNA sequence.
ACCESSION BI915586
VERSION BI915586.1 GI:16199311
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11608 row: i column: 12
High quality sequence stop: 716.
FEATURES Location/Qualifiers
source 1. .718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5241299"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTGCCACTCCCATTCTT 20
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Db 708 GCATTGCCACTCCCATTCTT 689

RESULT 34
BG695886/c
LOCUS BG695886 732 bp mRNA linear EST 07-MAY-2001
DEFINITION 602657850F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800708 5', mRNA sequence.
ACCESSION BG695886
VERSION BG695886.1 GI:13960469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10692  row: c  column: 13
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4800708"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        177 GCATTGCCACTCCCATTCTT 158


RESULT 35
BG194285/c
LOCUS       BG194285                743 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST13430 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG194285
VERSION     BG194285.1  GI:13715972
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        249 GCATTGCCACTCCCATTCTT 230


RESULT 36
BG695953/c
LOCUS       BG695953                743 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602657968F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800809 5',
            mRNA sequence.
ACCESSION   BG695953
VERSION     BG695953.1  GI:13960591
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10692  row: g  column: 18
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4800809"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        251 GCATTGCCACTCCCATTCTT 232


RESULT 37
CR383515/c
LOCUS       CR383515                747 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  CR383515 Bovine multi-stage muscles library (bcaj) Bos taurus cDNA
            clone bcaj0001a.d.01 5prim, mRNA sequence.
ACCESSION   CR383515
VERSION     CR383515.1  GI:47005419
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Chevalet,C.
  TITLE     AGENAE, a French Animal Genome project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Martin P
            INRA, Genomique & Physiologie de la Lactation
            Domaine de Vilvert, 78352 JOUY-EN-JOSAS cedex, FRANCE
            Tel: +33 (0) 1.34.65.25.82
            Fax: +33 (0) 1.34.65.29.26
            Email: Patrice.Martin@jouy.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0001  row: d  column: 1.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="bcaj0001a.d.01"
                     /tissue_type="muscles : heart, longissimus thoracis,
                     semitendinosus, masseter, cutaneus trunci"
                     /dev_stage="from embryos to adults"
                     /clone_lib="Bovine multi-stage muscles library (bcaj)"
                     /note="Clone distribution : AGENAE Resource centre.
                     Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
                     Radiobiologie et Etude du genome (LREG), Domaine de
                     Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0)
                     1.34.65.28.02, +33 (0) 1.34.65.22.73"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 7;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        416 GCATTGCCACTCCCATTCTT 397


RESULT 38
BF980113
LOCUS       BF980113                762 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  602288115T1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4373955 3',
            mRNA sequence.
ACCESSION   BF980113
VERSION     BF980113.1  GI:12347328
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 762)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10036  row: n  column: 04
            High quality sequence start: 25
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
     source          1. .762
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4373955"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation).  Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        543 GCATTGCCACTCCCATTCTT 562


RESULT 39
BG739895/c
LOCUS       BG739895                776 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602630838F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776320 5',
            mRNA sequence.
ACCESSION   BG739895
VERSION     BG739895.1  GI:14050548
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10628  row: k  column: 09
            High quality sequence stop: 776.
FEATURES             Location/Qualifiers
     source          1. .776
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4776320"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 776;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
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                    ||||||||||||||||||||
Db          87 GCATTGCCACTCCCATTCTT 68


RESULT 40
BG697487/c
LOCUS       BG697487                781 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602660680F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4804074 5',
            mRNA sequence.
ACCESSION   BG697487
VERSION     BG697487.1  GI:13963760
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10700  row: o  column: 19
            High quality sequence stop: 781.
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4804074"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 781;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        361 GCATTGCCACTCCCATTCTT 342


RESULT 41
BG189090/c
LOCUS       BG189090                789 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST8128 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG189090
VERSION     BG189090.1  GI:13710777
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 556.
FEATURES             Location/Qualifiers
     source          1. .789
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 4;  Length 789;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        279 GCATTGCCACTCCCATTCTT 260


RESULT 42
BG212376/c
LOCUS       BG212376                800 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST31963 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG212376
VERSION     BG212376.1  GI:13734063
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 800)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 408.
FEATURES             Location/Qualifiers
     source          1. .800
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
```

cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 800;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        271 GCATTGCCACTCCCATTCTT 252
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RESULT 43
BG865428/c
LOCUS BG865428 800 bp mRNA linear EST 29-MAY-2001
DEFINITION 602783545F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909906 5', mRNA sequence.
ACCESSION BG865428
VERSION BG865428.1 GI:14215968
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10809 row: i column: 11
High quality sequence stop: 800.
FEATURES Location/Qualifiers
source 1. .800
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4909906"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 800;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        444 GCATTGCCACTCCCATTCTT 425
```

RESULT 44
BI247050/c
LOCUS BI247050 809 bp mRNA linear EST 17-JUL-2001
DEFINITION 602960387F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5126204 5', mRNA sequence.
ACCESSION BI247050
VERSION BI247050.1 GI:14791603
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 809)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11308 row: m column: 21
High quality sequence stop: 787.
FEATURES Location/Qualifiers
source 1. .809
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5126204"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 809;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        648 GCATTGCCACTCCCATTCTT 629
```

RESULT 45
BU541989/c
LOCUS BU541989 816 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10252853 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6573777 5', mRNA sequence.
ACCESSION BU541989
VERSION BU541989.1 GI:22852472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 816)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2768 row: a column: 09
High quality sequence stop: 673.
FEATURES Location/Qualifiers
source 1. .816
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6573777"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 816;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCATTGCCACTCCCATTCTT 20
              ||||||||||||||||||||
Db        394 GCATTGCCACTCCCATTCTT 375
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Job time : 3158 secs